

ALIGNMENTS

SUMMARIES						
	result No.	Score	Query Match	Length	DB	ID
G	1	2085	100.0	2085	6	CQ868309
G	2	2085	100.0	2235	6	CQ868307
G	3	1794.4	86.1	2208	6	CQ868305
G	4	334.6	16.0	3543	1	BTTOXD1
G	5	334.6	16.0	4253	1	BACISSH4
G	6	334.6	16.0	4451	6	I08083
G	7	334.6	16.0	4451	6	I09103
G	8	334.6	16.0	4934	6	E01676
G	9	334.6	16.0	127923	1	BTPBTOXIS
G	10	221.8	10.6	6009	1	BTB251977
G	11	202.8	9.7	434	1	DQ078744
G	12	190.8	9.7	4959	1	AF285775
G	13	180.4	8.7	3752	1	AB125059
G	14	170	8.2	3642	1	AB193814
G	15	161.2	7.7	4895	1	AF132928
G	16	159.6	7.7	127923	1	BTPBTOXIS
G	17	158	7.6	3753	1	BACM03
G	18	116.6	7.0	2756	1	EE00614
G	19	115.8	7.0	2756	1	M12662
G	20	115.8	7.0	2756	1	DNAA encodin
G	21	115.8	7.0	2756	1	F000614

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

FEATURES	Source	Qualifiers
		<p>1. 2085 <i>organism</i>= "Bacillus thuringiensis" <i>mol type</i>= "unassigned DNA" <i>db_xref</i>= "taxon:1428"</p>
CDS		<p>1. 2085 <i>note</i>= "unnamed protein product" <i>codon_start</i>= 1 <i>transl_table</i>= 11 <i>protein_id</i>= "CAH313950_1" <i>protein_id</i>= "GI:51998356" <i>translation</i>= "MCQGNTQYCDNFETASADTIAAVSGATIVSGTLLL SCPIGIGAIILISFGTGLITVFNPGAGEQDKTVWPKXNGKQFVPLTPE LDEGFRQIQLSNTALDDDRKLRLNQAPLPSQSLQDQATLKFRRPENV GFOLETTKTLIPIYAQANFHLLQGQALADEBNWADLHSQQLPNAGC JKEKNIPICKSYNCANTYREGKLKURNEPNMRWSLNDYRQMTTDLTDF RYKDSIGRIGGIKTELTRTEIYTFIPLNLAILEINUTRSCE EULIFTYQTMTCYGRVLGJANRNRSTAYTGTETIYGERTYGPPITKLIP TDRQVTPISPFNNPYFTINQIELYLNNSPSNKLTYSAGNLNSDKKTTD KLTIMPAIKGENSLDNTSKVIECPGHTCGNLYLQSOGRLEITCTPNS YATNGAGTMLNPLNLSITIPGIGIQQRQNTESGSTNNNNLQYGDGYFOQ ENNIPPFNRADYNSILIIDKEFIPITSYVRNREKORLETIQKIN TNNTEPATMOTD"</p>

OPTION

Query Match Best Local Similarity Matches 2055; Conservative	100.0% ; Score 2085; Pred. No. 1, 5e-271;	DB 6; Length 2085;	Qy	1021 AAAATGAAACCTACGGAAATCGTTAGTGTATAAGTAGACTACTAT 1080
0; Mismatches 0; Indels 0; Gaps 0;			Db	1021 ABBATTAACCTACGGAAATCGTTAGTGTATAAGTAGACTACTAT 1080
Qy	1 ATGTCGCAAGGATAACCATATGGTATAATTTCGAGACATTGCTGATACA 60		Qy	1081 GCTACGACAGGAACGAAATTATATGGAGAAGAACGGTCCAACACAAAAC 1140
Db	1 ATGTCGCAAGGATAACCATATGGTATAATTTCGAGACATTGCTGATACA 60		Db	1081 GCTACGACAGGAACGAAATTATATGGAGAAGAACGGTCCAACACAAAAC 1140
Qy	61 ATTCCTGCAGTTAGTGAGGTACTATGATCCGGTATCGGTATACTCGGATA 120		Qy	1141 TTAATACATTGAACTCTTAAGGTTCAATTGTAACGTAGATAAGTAACTCTACT 1200
Db	61 ATTCCTGCAGTTAGTGAGGTACTATGATCCGGTATCGGTATACTCGGATA 120		Db	1141 TTAATACATTGAACTCTTAAGGTTCAATTGTAACGTAGATAAGTAACTCTACT 1200
Qy	121 CTCACTTCATATCGGAACTGGAGATAATAGTGTCTATAATAATCTTTGGTAC 180		Qy	1201 TCCCCCTTCTTAACATACATTAACATTAACTTAACTTAAATAATTATCA 1260
Db	121 CTCACTTCATATCGGAACTGGAGATAATAGTGTCTATAATAATCTTTGGTAC 180		Db	1201 TCCCCCTTCTTAACATACATTAACATTAACTTAACTTAAATAATTATCA 1260
Qy	181 CTAATCACTGCTCTTGGCCCGGGAGAACAGAACATGGACACAATTATT 240		Qy	1261 CCTAGTATAAACTAACATATTCTAGCTGGGGAAATTCTTAATGATAAAAAACACT 1320
Db	181 CTAATCACTGCTCTTGGCCCGGGAGAACAGAACATGGACACAATTATT 240		Db	1261 CCTAGTATAAACTAACATATTCTAGCTGGGGAAATTCTTAATGATAAAAAACACT 1320
Qy	241 AAATGGGGAAATTTTGGTATAACACGGTTAACAGAACATAACGTAAGTA 300		Qy	1321 GATTTCGATTTCCTGTTAAAAAAAGACTGTAAACCAATTAACTCCAAATTTGTGTACCA 1380
Db	241 AAATGGGGAAATTTTGGTATAACACGGTTAACAGAACATAACGTAAGTA 300		Db	1321 GATTTCGATTTCCTGTTAAAAAAAGACTGTAAACCAATTAACTCCAAATTTGTGTACCA 1380
Qy	301 CAAACTTGAAGGATTAGACAAATAATTACAGGATTAATAGTGTATTGG 360		Qy	1381 AGCTTAAATGTTATAGTCATATTTCATCCCAGTTCTTATTAACTTCCTTAA 1440
Db	301 CAAACTTGAAGGATTAGACAAATAATTACAGGATTAATAGTGTATTGG 360		Db	1381 AGCTTAAATGTTATAGTCATATTTCATCCCAGTTCTTATTAACTTCCTTAA 1440
Qy	361 AGAAAATTAAAAGACTAACAGCTTACATGCCATTACACAAAGCT 420		Qy	1441 ATTGGATTAGGCCTAAATTATATACTAGCTGGACACAGTAGTGTGT 1500
Db	361 AGAAAATTAAAAGACTAACAGCTTACATGCCATTACACAAAGCT 420		Db	1441 ATTGGATTAGGCCTAAATTATATACTAGCTGGACACAGTAGTGTGT 1500
Qy	421 GCCTTGACTCTAAATAAGCTTGGAGATGGTICACATGATTATTGGAGAACATCT 480		Qy	1501 AATAGAAATAATGCAATTACAGATAAAATAATTACATGATCCAGGAACTAACGGTAAC 1560
Db	421 GCCTTGACTCTAAATAAGCTTGGAGATGGTICACATGATTATTGGAGAACATCT 480		Db	1501 AATAGAAATAATGCAATTACAGATAAAATAATTACATGATCCAGGAACTAACGGTAAC 1560
Qy	481 GGTTCCACACTGAAACACTATAAACGCTTAAACTCCATTATGGCCAACTGTAAAT 540		Qy	1561 ACTCTTGATACAAACCTAAAGTAACTGAAAGGACCTGGTCATACAGGAAACACTGGTT 1620
Db	481 GGTTCCACACTGAAACACTATAAACGCTTAAACTCCATTATGGCCAACTGTAAAT 540		Db	1561 ACTCTTGATACAAACCTAAAGTAACTGAAAGGACCTGGTCATACAGGAAACACTGGTT 1620
Qy	541 TTTCATTAAATTATTACACAGGCTGAAATTGGCTGATGAAATGGAGATA 600		Qy	1621 TATTACATTGAGCTTCGATACCTAAATGGTGTGAAATACTCTCTTCDATAATCT 1740
Db	541 TTTCATTAAATTATTACACAGGCTGAAATTGGCTGATGAAATGGAGATA 600		Db	1621 TATTACATTGAGCTTCGATACCTAAATGGTGTGAAATACTCTCTTCDATAATCT 1740
Qy	601 CATCCTTCACAAATTGAACTTAATGCTGGAACTCAGTGAATTCTTAAA 660		Qy	1681 TATTACATTGAGCTTCGATACCTAAATGGTGTGAAATACTCTCTTCDATAATCT 1740
Db	601 CATCCTTCACAAATTGAACTTAATGCTGGAACTCAGTGAATTCTTAAA 660		Db	1681 TATTACATTGAGCTTCGATACCTAAATGGTGTGAAATACTCTCTTCDATAATCT 1740
Qy	661 GAAATAATACCTAAATAATTAGTAACTTACACAGGCTAAATACTTAA 720		Qy	1741 CCTACAAATCAGGAACTTAATGGCTGAAATACCTACAGGAACTTACACCTTCTGGT 1800
Db	661 GAAATAATACCTAAATAATTAGTAACTTACACAGGCTAAATACTTAA 720		Db	1741 CCTACAAATCAGGAACTTAATGGCTGAAATACCTACAGGAACTTACACCTTCTGGT 1800
Qy	721 CTTCGAAACGAAACCTTAATGAGATGGACTATTATGTTAGTGTATACT 780		Qy	1801 ACAAATTATAATTTCTGTTAGGAGATTTCAGTAACTTTCAGTAACTTCAAGTACAGTA 1860
Db	721 CTTCGAAACGAAACCTTAATGAGATGGACTATTATGTTAGTGTATACT 780		Db	1801 ACAAATTATAATTTCTGTTAGGAGATTTCAGTAACTTTCAGTAACTTCAAGTACAGTA 1860
Qy	781 ATTACTGTTAGTGTACTTCGCTCAATTTCGTTAGTATAAGGATAAAAGT 840		Qy	1861 ACATTACCTTAAATGAAACATACATTATGAAATTTCTGTCAGTGTATACTTCAAGTACAGTA 1920
Db	781 ATTACTGTTAGTGTACTTCGCTCAATTTCGTTAGTATAAGGATAAAAGT 840		Db	1861 ACATTACCTTAAATGAAACATACATTATGAAATTTCTGTCAGTGTATACTTCAAGTACAGTA 1920
Qy	841 TCAATAGGAAATAGTGTGCAATTAAAGAACCTTAACTGAA 900		Qy	1921 ATTTTAATCTGATGAAATTTCTGTCAGTGTATACTTCAAGTACAGTA 1980
Db	841 TCAATAGGAAATAGTGTGCAATTAAAGAACCTTAACTGAA 900		Db	1921 ATTTTAATCTGATGAAATTTCTGTCAGTGTATACTTCAAGTACAGTA 1980
Qy	901 ATAAATTGTCACCGCTCTAGTTACCTTCGTTAGTATAATGGAAAT 960		Qy	1981 GAAAACAAATTAGAAACTATCCAAACAAATAATACATTTCACAAATCATACA 2040
Db	901 ATAAATTGTCACCGCTCTAGTTACCTTCGTTAGTATAATGGAAAT 960		Db	1981 GAAAACAAATTAGAAACTATCCAAACAAATAATACATTTCACAAATCATACA 2040
Qy	961 AATTAACCGTTAGGGCTTACCTTCGTTAGTATAATGGAAACTTATTTATACA 1020		Qy	2041 AAAATACTTAAATATGAAAGCCAAACACTATGATTGATTAA 2085
Db	961 AATTAACCGTTAGGGCTTACCTTCGTTAGTATAATGGAAACTTATTTATACA 1020		Db	2041 AAAATACTTAAATATGAAAGCCAAACACTATGATTGATTAA 2085

'note="g was a in [1]"
'citation=[2]

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 /note="1976 bp downstream of HindIII site"
 381 . . 385
 /note="Shine-Dalgarno sequence"
 393 . . 395
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 /db_xref="GI: 216290"
 /translation="MNPQNKQKNEYETINASQKLNISNNYTPPIENSPIKLOLSTYKWDLNMCQNOQYGGDPEFTISGELSAYTIVGTVLTFGTGTTPLGLLJPGFTLIPVLFPAQDSNTSDEFTOTKNLKEASTYNSANKLNLSFNVNISTYHNLKTWENNPNQONTODVRLVYHTRVNPILVNPSPNPSDCDYNLVISSHQAQNLHTVLNQAVKPEAFLKNNRQFDYELPLPATAIDYPPVLTUAEIDTYNCVTCYTKGLNLJKTPTDSNLDGNIINNTNTYMTYRTRMTTAVIDLVLPFNPNDVGKPIGVOSELTRTEYCVLNFEBESPKYDQYQEDSLTRPHLFWLDSINFYEAQTFNFTHNNHFTYLNSQKSSYFGNINVTIDKLKSLGATNYTFLNVLNISLDKNUYNDANNISMDMFITINGTRILEKLTAGSGQITDVNKQIFGLPKREBNGNQPTLFPTDYNHSHLSPFIKSLISIPTVKUTVYTFATHSSVDPRTIYTHQVLSLQSKTAKVQHGFQHPTGDSLIDPKDHFKITCQHSNFOOSYFIRYASNGSANTRAVINLSPGVALGMALNPFTSGTDYTNLKYKDQVLESNVEKAAPQNQNLISLVRNRSSDVYNTVLDIKIEFLPITRSRERBEBKQJLBTQQLINTFYANIKTQLSLETDI DIOQDFTKFGHLNGSGARDIDGTFPTV1POKIDESKLKPPTVLYRSEFVGSSKDVELYVSRGEEIDAIMNPADLNYLPTSFDEGSRCETSAVANGNTSMLISQYDQKRNQVFCQSHQFSPTIDQALDTNENIGWVNMKIISSDGVSLDNLDIEVGPIDGBSLSVKQHMKWQNEAKRSENQVADVAKGADIALFTNVDEALDFDTIAQIOYAEVLYNOSIPTVYNDLSDVPGMNDIYVLDARYAQARLYLDFQVGMWHVIGNADQOIDGUSVULNSNSAGSONVHLOHNHGTVLRVIAKKGPGNGVYTMDCBEEQEKLJFTSCEBEGYTKTVDFVPDTDRVIEIGETEGSYIESIELCME"

ORIGIN

| Query | Match | Score | Length | DB | 1: | 2: | 3: | 4: | 5: | 6: | 7: | 8: | 9: | 10: | 11: | 12: | 13: | 14: | 15: | 16: | 17: | 18: | 19: | 20: | 21: | 22: | 23: | 24: | 25: | 26: | 27: | 28: | 29: | 30: | 31: | 32: | 33: | 34: | 35: | 36: | 37: | 38: | 39: | 40: | 41: | 42: | 43: | 44: | 45: | 46: | 47: | 48: | 49: | 50: | 51: | 52: | 53: | 54: | 55: | 56: | 57: | 58: | 59: | 60: | 61: | 62: | 63: | 64: | 65: | 66: | 67: | 68: | 69: | 70: | 71: | 72: | 73: | 74: | 75: | 76: | 77: | 78: | 79: | 80: | 81: | 82: | 83: | 84: | 85: | 86: | 87: | 88: | 89: | 90: | 91: | 92: | 93: | 94: | 95: | 96: | 97: | 98: | 99: | 100: | 101: | 102: | 103: | 104: | 105: | 106: | 107: | 108: | 109: | 110: | 111: | 112: | 113: | 114: | 115: | 116: | 117: | 118: | 119: | 120: | 121: | 122: | 123: | 124: | 125: | 126: | 127: | 128: | 129: | 130: | 131: | 132: | 133: | 134: | 135: | 136: | 137: | 138: | 139: | 140: | 141: | 142: | 143: | 144: | 145: | 146: | 147: | 148: | 149: | 150: | 151: | 152: | 153: | 154: | 155: | 156: | 157: | 158: | 159: | 160: | 161: | 162: | 163: | 164: | 165: | 166: | 167: | 168: | 169: | 170: | 171: | 172: | 173: | 174: | 175: | 176: | 177: | 178: | 179: | 180: | 181: | 182: | 183: | 184: | 185: | 186: | 187: | 188: | 189: | 190: | 191: | 192: | 193: | 194: | 195: | 196: | 197: | 198: | 199: | 200: | 201: | 202: | 203: | 204: | 205: | 206: | 207: | 208: | 209: | 210: | 211: | 212: | 213: | 214: | 215: | 216: | 217: | 218: | 219: | 220: | 221: | 222: | 223: | 224: | 225: | 226: | 227: | 228: | 229: | 230: | 231: | 232: | 233: | 234: | 235: | 236: | 237: | 238: | 239: | 240: | 241: | 242: | 243: | 244: | 245: | 246: | 247: | 248: | 249: | 250: | 251: | 252: | 253: | 254: | 255: | 256: | 257: | 258: | 259: | 260: | 261: | 262: | 263: | 264: | 265: | 266: | 267: | 268: | 269: | 270: | 271: | 272: | 273: | 274: | 275: | 276: | 277: | 278: | 279: | 280: | 281: | 282: | 283: | 284: | 285: | 286: | 287: | 288: | 289: | 290: | 291: | 292: | 293: | 294: | 295: | 296: | 297: | 298: | 299: | 300: | 301: | 302: | 303: | 304: | 305: | 306: | 307: | 308: | 309: | 310: | 311: | 312: | 313: | 314: | 315: | 316: | 317: | 318: | 319: | 320: | 321: | 322: | 323: | 324: | 325: | 326: | 327: | 328: | 329: | 330: | 331: | 332: | 333: | 334: | 335: | 336: | 337: | 338: | 339: | 340: | 341: | 342: | 343: | 344: | 345: | 346: | 347: | 348: | 349: | 350: | 351: | 352: | 353: | 354: | 355: | 356: | 357: | 358: | 359: | 360: | 361: | 362: | 363: | 364: | 365: | 366: | 367: | 368: | 369: | 370: | 371: | 372: | 373: | 374: | 375: | 376: | 377: | 378: | 379: | 380: | 381: | 382: | 383: | 384: | 385: | 386: | 387: | 388: | 389: | 390: | 391: | 392: | 393: | 394: | 395: | 396: | 397: | 398: | 399: | 400: | 401: | 402: | 403: | 404: | 405: | 406: | 407: | 408: | 409: | 410: | 411: | 412: | 413: | 414: | 415: | 416: | 417: | 418: | 419: | 420: | 421: | 422: | 423: | 424: | 425: | 426: | 427: | 428: | 429: | 430: | 431: | 432: | 433: | 434: | 435: | 436: | 437: | 438: | 439: | 440: | 441: | 442: | 443: | 444: | 445: | 446: | 447: | 448: | 449: | 450: | 451: | 452: | 453: | 454: | 455: | 456: | 457: | 458: | 459: | 460: | 461: | 462: | 463: | 464: | 465: | 466: | 467: | 468: | 469: | 470: | 471: | 472: | 473: | 474: | 475: | 476: | 477: | 478: | 479: | 480: | 481: | 482: | 483: | 484: | 485: | 486: | 487: | 488: | 489: | 490: | 491: | 492: | 493: | 494: | 495: | 496: | 497: | 498: | 499: | 500: | 501: | 502: | 503: | 504: | 505: | 506: | 507: | 508: | 509: | 510: | 511: | 512: | 513: | 514: | 515: | 516: | 517: | 518: | 519: | 520: | 521: | 522: | 523: | 524: | 525: | 526: | 527: | 528: | 529: | 530: | 531: | 532: | 533: | 534: | 535: | 536: | 537: | 538: | 539: | 540: | 541: | 542: | 543: | 544: | 545: | 546: | 547: | 548: | 549: | 550: | 551: | 552: | 553: | 554: | 555: | 556: | 557: | 558: | 559: | 560: | 561: | 562: | 563: | 564: | 565: | 566: | 567: | 568: | 569: | 570: | 571: | 572: | 573: | 574: | 575: | 576: | 577: | 578: | 579: | 580: | 581: | 582: | 583: | 584: | 585: | 586: | 587: | 588: | 589: | 590: | 591: | 592: | 593: | 594: | 595: | 596: | 597: | 598: | 599: | 600: | 601: | 602: | 603: | 604: | 605: | 606: | 607: | 608: | 609: | 610: | 611: | 612: | 613: | 614: | 615: | 616: | 617: | 618: | 619: | 620: | 621: | 622: | 623: | 624: | 625: | 626: | 627: | 628: | 629: | 630: | 631: | 632: | 633: | 634: | 635: | 636: | 637: | 638: | 639: | 640: | 641: | 642: | 643: | 644: | 645: | 646: | 647: | 648: | 649: | 650: | 651: | 652: | 653: | 654: | 655: | 656: | 657: | 658: | 659: | 660: | 661: | 662: | 663: | 664: | 665: | 666: | 667: | 668: | 669: | 670: | 671: | 672: | 673: | 674: | 675: | 676: | 677: | 678: | 679: | 680: | 681: | 682: | 683: | 684: | 685: | 686: | 687: | 688: | 689: | 690: | 691: | 692: | 693: | 694: | 695: | 696: | 697: | 698: | 699: | 700: | 701: | 702: | 703: | 704: | 705: | 706: | 707: | 708: | 709: | 710: | 711: | 712: | 713: | 714: | 715: | 716: | 717: | 718: | 719: | 720: | 721: | 722: | 723: | 724: | 725: | 726: | 727: | 728: | 729: | 730: | 731: | 732: | 733: | 734: | 735: | 736: | 737: | 738: | 739: | 740: | 741: | 742: | 743: | 744: | 745: | 746: | 747: | 748: | 749: | 750: | 751: | 752: | 753: | 754: | 755: | 756: | 757: | 758: | 759: | 760: | 761: | 762: | 763: | 764: | 765: | 766: | 767: | 768: | 769: | 770: | 771: | 772: | 773: | 774: | 775: | 776: | 777: | 778: | 779: | 780: | 781: | 782: | 783: | 784: | 785: | 786: | 787: | 788: | 789: | 790: | 791: | 792: | 793: | 794: | 795: | 796: | 797: | 798: | 799: | 800: | 801: | 802: | 803: | 804: | 805: | 806: | 807: | 808: | 809: | 810: | 811: | 812: | 813: | 814: | 815: | 816: | 817: | 818: | 819: | 820: | 821: | 822: | 823: | 824: | 825: | 826: | 827: | 828: | 829: | 830: | 831: | 832: | 833: | 834: | 835: | 836: | 837: | 838: | 839: | 840: | 841: | 842: | 843: | 844: | 845: | 846: | 847: | 848: | 849: | 850: | 851: | 852: | 853: | 854: | 855: | 856: | 857: | 858: | 859: | 860: | 861: | 862: | 863: | 864: | 865: | 866: | 867: | 868: | 869: | 870: | 871: | 872: | 873: | 874: | 875: | 876: | 877: | 878: | 879: | 880: | 881: | 882: | 883: | 884: | 885: | 886: | 887: | 888: | 889: | 890: | 891: | 892: | 893: | 894: | 895: | 896: | 897: | 898: | 899: | 900: | 901: | 902: | 903: | 904: | 905: | 906: | 907: | 908: | 909: | 910: | 911: | 912: | 913: | 914: | 915: | 916: | 917: | 918: | 919: | 920: | 921: | 922: | 923: | 924: | 925: | 926: | 927: | 928: | 929: | 930: | 931: | 932: | 933: | 934: | 935: | 936: | 937: | 938: | 939: | 940: | 941: | 942: | 943: | 944: | 945: | 946: | 947: | 948: | 949: | 950: | 951: | 952: | 953: | 954: | 955: | 956: | 957: | 958: | 959: | 960: | 961: | 962: | 963: | 964: | 965: | 966: | 967: | 968: | 969: | 970: | 971: | 972: | 973: | 974: | 975: | 976: | 977: | 978: | 979: | 980: | 981: | 982: | 983: | 984: | 985: | 986: | 987: | 988: | 989: | 990: | 991: | 992: | 993: | 994: | 995: | 996: | 997: | 998: | 999: | 1000: | 1001: | 1002: | 1003: | 1004: | 1005: | 1006: | 1007: | 1008: | 1009: | 1010: | 1011: | 1012: | 1013: | 1014: | 1015: | 1016: | 1017: | 1018: | 1019: | 1020: | 1021: | 1022: | 1023: | 1024: | 1025: | 1026: | 1027: | 1028: | 1029: | 1030: | 1031: | 1032: | 1033: | 1034: | 1035: | 1036: | 1037: | 1038: | 1039: | 1040: | 1041: | 1042: | 1043: | 1044: | 1045: | 1046: | 1047: | 1048: | 1049: | 1050: | 1051: | 1052: | 1053: | 1054: | 1055: | 1056: | 1057: | 1058: | 1059: | 1060: | 1061: | 1062: | 1063: | 1064: | 1065: | 1066: | 1067: | 1068: | 1069: | 1070: | 1071: | 1072: | 1073: | 1074: | 1075: | 1076: | 1077: | 1078: | 1079: | 1080: | 1081: | 1082: | 1083: | 1084: | 1085: | 1086: | 1087: | 1088: | 1089: | 1090: | 1091: | 1092: | 1093: | 1094: | 1095: | 1096: | 1097: | 1098: | 1099: | 1100: | 1101: | 1102: | 1103: | 1104: | 1105: | 1106: | 1107: | 1108: | 1109: | 1110: | 1111: | 1112: | 1113: | 1114: | 1115: | 1116: | 1117: | 1118: | 1119: | 1120: | 1121: | 1122: | 1123: | 1124: | 1125: | 1126: | 1127: | 1128: | 1129: | 1130: | 1131: | 1132: | 1133: | 1134: | 1135: | 1136: | 1137: | 1138: | 1139: | 1140: | 1141: | 1142: | 1143: | 1144: | 1145: | 1146: | 1147: | 1148: | 1149: | 1150: | 1151: | 1152: | 1153: | 1154: | 1155: | 1156: | 1157: | 1158: | 1159: | 1160: | 1161: | 1162: | 1163: | 1164: | 1165: | 1166: | 1167: | 1168: | 1169: | 1170: | 1171: | 1172: | 1173: | 1174: | 1175: | 1176: | 1177: | 1178: | 1179: | 1180: | 1181: | 1182: | 1183: | 1184: | 1185: | 1186: | 1187: | 1188: | 1189: | 1190: | 1191: | 1192: | 1193: | 1194: | 1195: | 1196: | 1197: | 1198: | 1199: | 1200: | 1201: | 1202: | 1203: | 1204: | 1205: | 1206: | 1207: | 1208: | 1209: | 1210: | 1211: | 1212: | 1213: | 1214: | 1215: | 1216: | 1217: | 1218: | 1219: | 1220: | 1221: | 1222: | 1223: | 1224: | 1225: | 1226: | 1227: | 1228: | 1229: | 1230: | 1231: | 1232: | 1233: | 1234: | 1235: | 1236: | 1237: | 1238: | 1239: | 1240: | 1241: | 1242: | 1243: | 1244: | 1245: | 1246: | 1247: | 1248: | 1249: | 1250: | 1251: | 1252: | 1253: | 1254: | 1255: | 1256: | 1257: | 1258: | 1259: | 1260: | 1261: | 1262: | 1263: | 1264: | 1265: | 1266: | 1267: | 1268: | 1269: | 1270: | 1271: | 1272: | 1273: | 1274: | 1275: |
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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | 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RESULT 6	108083	108083	Sequence 1 from Patent EP 02966870.	4451 bp	DNA	linear	PAT 02-DEC-1994	
DEFINITION	ACCESSION	VERSION	New toxin-encoding DNA fragments from <i>Bacillus thuringiensis</i> subsp. <i>israelensis</i>	EP 02966870-A1 1 28-DEC-1988;				
KEYWORDS	ORGANISM	SOURCE	Unknow.	Author.D.J. and Ward.E.S.				
REFERENCE	1. (bases 1 to 4451)	2. (bases 36 to 4451)	3. (bases 636 to 651)	4. (bases 1 to 451)	5. (bases 1 to 451)	6. (bases 1 to 451)	7. (bases 1 to 451)	8. (bases 1 to 451)
AUTHORS	JOURNAL	FEATURES	source	Patent	Location/Qualifiers	organism="unknown"	/mol_type="unassigned DNA"	
ORGANISM	TITLE	source	ORIGIN	Query Match	Score 334.6; DB 6; Length 4451;			
DEFINITION	DEFINITION	DEFINITION	DEFINITION	Best Local Similarity	53.9%; Pred. No. 4.4e-36;	Indels	38; Gaps	7;
ACCESSION	ACCESSION	ACCESSION	ACCESSION	Matches	858; Conservative	0; Mismatches	635;	
VERSION	VERSION	VERSION	VERSION	Qy	499 TATAAACGCTTAATCAGTCACTTTATGCCAAGCTGCTTAATTTCATTAAATTATA 558	Db	2489 TTATACACATTAAACCCAAATTCCAGCTGTAACCTGGACTTGCTGGACTGTTC 2548	
KEYWORDS	KEYWORDS	KEYWORDS	KEYWORDS	Qy	1494 TATAAACCATATCAGTCACTTTATGCCAAGCTGCTTAATTTCATTAAATTATA 1553	Db	2549 TAAGGTGTTAGGACTGGCTCATAGGCTGGCATACAGGAAACTGGTTTACAAAGTC 1577	
SOURCE	SOURCE	SOURCE	SOURCE	Qy	559 CACAAGTGTGAATGGCTGATGAATGAAATGCAAAATTCAAAATTGAA 618	Db	1458 TATATATATACAGGTCATTAGGAGCACACAGTCACTGTTAAATGAAATGAA 1517	
ORGANISM	ORGANISM	ORGANISM	ORGANISM	Db	1554 ATCAAGCGCTGAATTQAAGCTTAAACATGACATGACATTGATTTAGAG 1613	Db	2429 TAAAACCTCAAGTGTCAACACTGGTAAATGAAATGAAATGAAATGAA 2488	
DEFINITION	DEFINITION	DEFINITION	DEFINITION	Qy	619 CCTPATGCTGGAAATCATAGTCACTTTAAAGAAATAATACCTAAATAT 678	Db	1518 ATCAGTAAATAATTACATGATCCAGCATCAAGGTACAGCTGTTGATCAAACCTC 1577	
ACCESSION	ACCESSION	ACCESSION	ACCESSION	Db	1614 CCTTGCC--AACGCAATTGATTATTCAGTATGACTAAAGTAAAGTAGATTAC 1670	Db	2489 TTATGCCTCAATGGAAAGCCTAAATCTGAGCTGTTAGATGAAATGAA 2606	
VERSION	VERSION	VERSION	VERSION	Qy	679 AATPACATTTGCAAAATPACCTATGAGAAGGCTAAATAACTCGAAAGBACCTAA 738	Db	1638 GCGTTTAGAGATTACATGTAGAAATCTACACAATCTTAACTTAACTGTTGCTCG 1697	
KEYWORDS	KEYWORDS	KEYWORDS	KEYWORDS	Db	1671 ACTAATTATTTGCTAACACTTAAATAAAGGATTAAATTAAACAGCCTGAT 1730	Db	2663 TTATGCCTCAATGGAAAGCCTAAATCTGAGCTGTTAGATGAAATGAA 2722	
SOURCE	SOURCE	SOURCE	SOURCE	Qy	739 ATGAGATGGAGTATATTAATGATTATGAGATATGACTATTACTGTTAGATCT 798	Db	1758 AATAGGAAATACCCTAACGACTCAAAACACTTTCTGTTAGGAAATGAA 1817	
ORGANISM	ORGANISM	ORGANISM	ORGANISM	Db	1731 AATPACTCTGATGCGAAATTAAACTGGAAACATACATACCTATGAAACAAATTGACT 1790	Db	2723 AGCAGACTG--GGPATGGCACTCAACCCACTTTCTGTTAGGATTTACGGATT 2779	
DEFINITION	DEFINITION	DEFINITION	DEFINITION	Qy	799 ATCGCTCAATTTCCTTTATGATTAAGAGATAACAGATTCAATGGAGAATAGGT 858	Db	2663 TTATGCCTCAATGGAAAGCCTAAATCTGAGCTGTTAGATGAAATGAA 2839	
ACCESSION	ACCESSION	ACCESSION	ACCESSION	Db	1791 ACGTGTGTTAGATGTTGCACTCTTCCTTAATTATGAGTTAGTAATATCCATA 1850	Db	1878 AAACATACCCATTATTTAACTGTCAGATGTT--CAAATTCAATTTCTGTTAGT 1934	
VERSION	VERSION	VERSION	VERSION	Qy	859 GGATTAATAAACTGAAACTTCAAGAGAAATTATACAACTGAAATAATTGACCCCTCT 918	Db	2840 AAACATACCTCTGTTAAATCGTGTGGATTATAACACACAGTACTTTGATTTGTA 2899	
KEYWORDS	KEYWORDS	KEYWORDS	KEYWORDS	Db	1851 GTGTGCTCAATTCTGCAACTCTGAAATTAT-----CAGGTACTTCACTTCGAGA 1903	Db	1935 TAAATGAAATTATACAAATTACTPCTCTGTTAGGAAACAAATT 1994	
SOURCE	SOURCE	SOURCE	SOURCE	Qy	919 ACTTACCTTGAAATTCAACCCAACTCTCCATTATGGAAATAATACAGCTTCTGG 978	Db	2900 TAAATGAAATTCTGCAAAACTTACATTTTCAGAAATCATACAAATGAAACAAATT 2959	
ORGANISM	ORGANISM	ORGANISM	ORGANISM	Db	1904 AGGCCCTTAATTAATATGACTTTCAATATCAAGAGSGATTCACCTTACAGCGCA 1963	Db	1995 AGAAACATCTCAACAAAAATAATCATTTTCAGAAATCATACAAATGAAACAAATT 2054	
DEFINITION	DEFINITION	DEFINITION	DEFINITION	Qy	979 CTGAGATTATTCTCATTTAGTAAGACTTATTAATACAGAAATAATGAAAGCTGAGGG 1038	Db	2960 AGAAAAGTACACAAATAATTATGAAATTTGCAATGACATTTGAACTTACA 3050	
ACCESSION	ACCESSION	ACCESSION	ACCESSION	Db	1954 TTATTTACTTGGCTTGTGTTGAAATTATGAAAGGCGCARACTCTCTAAATA 2023	Db	3020 ATCAGAAACTTACAGATTAGACATAGACATAGACATAGACATAGACATAGACAA 3050	
VERSION	VERSION	VERSION	VERSION	Qy	10139 AATCGTTTGTGTTGCTTATGGCTTAATGATCTACTTATGCTGACAGGAACTGA 1097	Db	RESULT 7	
KEYWORDS	KEYWORDS	KEYWORDS	KEYWORDS	Db	2024 TTTTTCACCGCCATTATAATATGTTCACTGATAATATCCAAAATAC 2083	Db	109103 Locus Sequence 1 from Patent WO 8810305.	
SOURCE	SOURCE	SOURCE	SOURCE	Qy	1008 AATATATATGGCAAAAGAACAGSTGCCACCCACACAAACTTTAACTCCATTGAACT 1157	Db	109103 Definition Version 109103 GI: 588188	
ORGANISM	ORGANISM	ORGANISM	ORGANISM	Db	2084 TAGTGTGTTGAAATCACAACTTAACTGATAATTTCTGCTTGGCAAGAAA 2143	Db	109103 Organism Unknown.	
DEFINITION	DEFINITION	DEFINITION	DEFINITION	Qy	1158 CTATAAAAGTTCAATTGTAAGCTGAACTGAACTCCACTTCCCTTTCTAACT 1217	Db	109103 Classification Unclassified.	
ACCESSION	ACCESSION	ACCESSION	ACCESSION	Db	2144 TATTATATTTTATTAATGTCATAGCTTGTGAAATTATGAAATTAATGATTTAA 2203	Db	109103 Reference 1 (bases 1 to 4451)	

AUTHORS	Ellar, D.J. and Ward, E.S.
JOURNAL	WO 810305 A 1 29-DEC-1988;
FEATURES	Location/Qualifiers
source	1..4451/ organism="unknown" /mol_type="unassigned DNA"
ORIGIN	
Query Match 16.0%; Score 334.6; DB 6; Length 4451;	
Best Local Similarity 53.9%; Pred. No. 4.4e-36;	
Matches 858; Conservative 0; Mismatches 695; Indels 38; Gaps 7;	
499 TATAAACGCTTAACTCATTGCGAGCTCAATTTCATTAATTATTA 558	Db 2384 TCATATTTTATCATTTAATTTAGCTTGTATCCCT-----TGCAACATC 1577
1494 TATAACATACATGATTATCTAGTATGCAAGCAGAAACTACATGCTTAA 1553	Qy 1458 TATATATATAAGGTGCAATTAGGTGACAGCTAGTTAAATGCAAT 1517
559 CAACANGGTGCTGAATTGGCTGATGATGGATGCGATATACTCCTCACAAATTGAA 618	Db 2429 TAABACTCAACTGTGATGCGACTCTAGTGTGACACTGATGCTAAATGATC 2488
1554 AATCAAGCGTCAAATTGAACTGGTAAATTAACATGCAAAATTGAG 1613	Qy 1518 ATCAGATAAAAATTAATCATGATCCAGCAATCAAGGTTAATGAAAGT 1577
619 CCTAATGCTGGACATCAGATGACTATTAAACCTTTAAAGAAATAACCTTAATAAT 678	Db 2489 TTATACACATTAACCTCCAAATTCCAGCTGTAANAGGATTAAATGATCCTGGCTTC 2548
1614 CTTTGCC--AACAGCAATTGATTATTCAGTAAAGCTATAAGGATTAC 1670	Qy 1578 TAAGGTTAATGGAGGACCTGATGACTCTAACTCTTAACTGAACTTCAAGGAG 1637
679 AGTAACATTGTGCCAAATACCTATAGAAGGACTATAAACTCCAAACCTTAAT 738	Db 2549 TAAGGTGTTGAGGTTAATGGTTAAATGTTCAAGGTTCAAGGAG 2605
1671 ACTAAATTGTGTAACACTTAAAGGATTAAATTATTAACAGGCTCTGA 1730	Qy 1538 GCGTTTGGAGGATTACTGTGAGACTCTAACTCTTAACTGAACTTCAACAACTTCAAACTCTTCAACACTTCAAACTGTTTATAGATTCG 1697
739 ATGAGATGGAGPATATTATGATTATCGAAAGATAATGACTPATTACTGTTAATGATACT 798	Db 2606 ---TTCTRAAAATTACATGTCACACTCAAACTTCAACACTTCAAACTGTTTATAGATTCG 2662
1731 AGTAATCTTGATGCAAAATTAAACTGGAAACATACTGATTCACAAAAAATGACT 1790	Qy 1698 ATACGGTACAATGCTGGAAATAACTCTCTTAATATCTCAATACGGAGGT 1757
799 ATCGCTCAATTCTCTTTATGATATAAGAGATAACGATCAATAGGAAATAGT 858	Db 2663 TTATGCTCRAATGGCAAGTAACTGCGCTGTTAATCTAGTGTGCGCTGT 2722
1791 ACTGCTGTTATTAGATGTTGACTCTTCTCTTAATGATGATGCTTAATPATCCAAATA 1850	Qy 1758 AATAGAATACACCCCTAACAGACTCAAACACTTCTGTTCAAGTAACTTAAATTAATTT 1817
859 GGCTTAAAACTGAACITCAAGAGAAATTATACAACTGAAATAATTTCACCGCTCT 918	Db 2723 AGAGAACTG---GGTAGGGACTCAACCCACTTTCTGTAAGGTTACAGTAACTGATTGATT 2779
1851 GTGTGCCATTCTGAACTACTCTGAGAAATTATTCAGGTTAATCTCGAGA 1903	Qy 1818 ACAATACGGAGATTGGGTATTCCAAATTCCAGTAACTTAACTGAACTTAAATCTG 1877
919 ACTTACCTTGTGAAATTCAACCCAACTCTCGCTTAAATGGAAATAATTTAACCTCAGGG 978	Db 2780 AAAATATAAAGGTTTCAGTACTGTTCAAGGGTGAATTGGTCACAACTCA 2839
1904 AAGCCCTTATAAATATTAGCTTCAATTCAGAGATTCACTTACAGCTTAACT 1963	Qy 1878 AAACATACCATTTATTTAACTTAACTGTTAACTGAGATGTATCATGTTAATCTGTA 1934
979 CTAGAATTATTTTCATTTAGTGAACCTTATATTATACAAAAAATGAAAGTAACTGGG 1038	Db 2840 AACATATCTCTGTGTTTAATGCTGATGTTAATCACACAGTACTTATGTA 2899
1964 TTATTACTTGTGTTGATGTTGATGTTGATGTTGATGAAATTATGAGAAATTAT 2023	Qy 1935 TAAATGAAATTATACCAAAATTACTCTCTGTAAGCCAAAATAGAGAAAAACAAATAATT 1994
1039 AATGTTTGTGAAAGAACAGCTCCACCAAACTTCAATGAACTTCACTTCACT -ATGCTACGACGAACTG 1097	Db 2900 TAAATGAAATTCTGCAATTACTGTTCAAGGTTAATGAGGTTAGAGGATAGAGAAACAAATT 2959
2024 TTTCACAGCCATTATAATGTTTCACTTACACTGTATAATTCACCTAAAT 2083	Qy 1995 AGAAACATTCACAAACAAAAAAATATACATTTCACAAATCATCAAAATATCTTAAATCTTAACTTACA 2054
1098 AATTATATATGGAAAGAACAGCTCCACCAAACTTCAATGAACTTCACTTCACT 1157	Db 2960 AGAAACACTACACAAATAATTAACTTAACTTAACTTAACTTAACTTACA 2019
2084 TAGTGTGTTGAAATCAAAATGTTTCACTTACACTGTATAATTCACCTAAAT 2143	Qy 2055 TATAGAAGCCACAACTACTGATATTGATTAA 2085
1158 CTATAAAGTTTCATTGTTGAACTTACACTCCACTTCCCTTCTCAAT 1217	Db 3020 ATCAGAACTTACGATGTTGATGACATGATGAA 3050
2144 TATTATATTTTTTATTAATGCTCATAGCTTAAATATCTAAATGATTATA 2203	RESULT 8
2024 TTTCACAGCCATTATAATGTTTCACTTACACTGTATAATTCACCTAAAT 2083	E01676 4934 bp linear PAT 29-SEP-1997
1098 AATTATATATGGAAAGAACAGCTCCACCAAACTTCAATGAACTTCACT 1157	LOCUS DNA sequence encoding Bacillus thuringiensis insecticidous protein.
2084 TAGTGTGTTGAAATCAAAATGTTTCACTTACACTGTATAATTCACCTAAAT 2143	DEFINITION E01676
1158 CTATAAAGTTTCATTGTTGAACTTACACTCCACTTCCCTTCTCAAT 1217	VERSION E01676_1 GI:2169929
2144 TATTATATTTTTTATTAATGCTCATAGCTTAAATATCTAAATGATTATA 2203	KEYWORDS JP 1988230090-A 1 26-SEP-1988;
2264 TACAGCAGGATCTGGCAATAACTTATGTTAAATTTGGTTACCAT 2323.	SOURCE Bacillus thuringiensis
1218 ATACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 1277	ORGANISM Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus cereus group.
2204 TAATATTAGTAAATGGTATTAACTTAACTTAACTTAACTTAACTTAACT 2263	COMMENT PN JP 1988230090-A_1
1278 ATATTACGCTGGGGCAAAATTCTAATGATAAAAAACACTGATTTCAATTCTCTG 1337	PD 26-SEP-1988
1218 ATACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 1277	PP 19-MAR-1987 JP 1987066844
2204 TAATATTAGTAAATGGTATTAACTTAACTTAACTTAACTTAACTTAACT 2263	PI KOMANO TORU, HIMENO MICHIO
1278 ATATTACGCTGGGGCAAAATTCTAATGATAAAAAACACTGATTTCAATTCTCTG 1337	PC C12N15/00 A01NC63/00, C12P21/02//A01NC63/02, (C12N1/20, C1R1.19);
2264 TACAGCAGGATCTGGCAATAACTTATGTTAAATTTGGTTACCAT 2323.	CC strandedness: Double;
1338 AAAAAAAGCTGTTAACCAATTATAATCCAAATTTGTTACCAAGCTTATAATGTTAG 1397	topology: Linear;
2324 TCTTAAACGRAGAGRAAATCAAGGAAACCCCTTCCATAGATAACTATAG 2383	CC
1398 TCAATTATTCAGTTCTTATTAAATTCCTTAAATGZTTAGGCCTAA 1457	

CC	hypothetical: No;	Db	2742	TACGGGAGATCTGGAAATAACTATGTAATAATTTCGGTTACCAAT	2801
CC	anti-sense: No;	Qy	1338	AAAAAAGACTGTAACCAATTATTATCCTAAATTGTACCAAGCTATAAGTATAG	1397
* Source: Strain=HD522;	Location/Qualifiers	Db	2802	TCTTAACGAGAGAACTACCTACCCCTACCCCTACCAACATGATAACTATG	2861
Key		Qy	1398	TCATATTTCCTCCCASTTTCTTTAAATTCTATAAAAATTGATTAGCGCTAA	1457
FH		Db	2862	TCATATTTCATATTAAAGTCTAGATCCC-----TGCAACATA	2906
FH		Qy	1458	TATATATATACAGGTCATTAGGGACACAGTAGTGTAACTAGAAATAATGCAAT	1517
FT	5' UTR	Db	2907	AAAACCTCAAGTGTATAACGTTGACACTCTAGTGTGATCTGGACTGCTTC	2966
FT	CDS	Qy	1518	ATCAGATAAAATAATACAATGATCCAGCATACAGGTAACACTGGTTTACAAAGTCAGG	1577
FT	/product= 'Bacillus thuringiensis insectivorous protein'.	Db	2967	TTATACATTTAACCTCCAAATTCTGAGTAAAGGATTAAAGCTTGATCAAGATCA	3026
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Query Match	Match	Db	3027	TAAGGTGTTCAAGGCTGGFCATAGGGGTTATTGATTGATTCAGGAGATCA	3083
Best Local Similarity	Score	Qy	1588	GGGTAGAGATTACATGTAGAACTCTAACTACATCTACAACTCTTACATTAGA	1697
Matches	58;	Db	3084	--TRICAAAAATTACTGTCAACACTCAAATTTCACAATGTTTATAGATTGTC	3140
Conservative	0;	Qy	1698	ATACGTCAAAATGGGTGGAATAATCTCTCTTACATACTGTTACAACTGGAGT	1757
Mismatches	659;	Db	3141	TTATGGTTCAAATGGAGGCAAAATTCTGAGCTGTGTTAAATCTGTTACGGGT	3200
Indels	38;	Qy	1758	AATAGGAAATCCACCTCAACGACTCAACAAACCTTTCTGGTACAAATTAAATA	1817
Gaps	7;	Db	3201	ACGAGACTG--GGPATGGACTCACCCACTTTCGGTACAGTTACGATTACGATT	3257
		Qy	1818	ACAATAGGAGATTGGTATTCCAAATTCCAAGTAACTTACCTTTAAATG	1877
		Db	3258	AAAATAAAAGATTTCAGTACTGAAATTCTGAGTTCTACGAGGTGAATTGTC	3317
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		Qy	1935	AAAATTGAAATTACCAATTACTTCCCTCTGTAACCCAAATAATGAGAAACAAATT	1994
		Db	3378	TAAATGAAATTCTGCAAAATTACTGTTTAAAGGAGTATGAGAACAAATT	3437
		Qy	1995	AGAAACTATCCRAACAAAATAATTATCATTTCACAAATCATACAAAAAAAT	2054
		Db	3438	AGAAAATGTAACAAATAATTACATTTATGAAATCATTTATGCAAA	3497
		Qy	2055	TATAGAAGGCCAAATTATGATGTTAA	2085
		Db	3498	ATCAGAACTTACAGATTGACATAGATGACATAGATCAA	3528
ORIGIN		RESULT 9			
		BTBTOXIS	127923 bp	DNA	linear
		LOCUS	Bacillus thuringiensis subsp. israelensis plasmid pBtoxis.		
		DEFINITION	Bacillus thuringiensis serovar israelensis		
		ACCESSION	AL731825		
		VERSION	AL731825.1	GI:21685410	
		KEYWORDS			
		SOURCE	Bacillus thuringiensis serovar israelensis		
		ORGANISM	Bacillus thuringiensis serovar israelensis		
		BACTERIA	Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.		
		REFERENCE	1 (bases 1 to 127923)		
		AUTHORS	Berry, C., O'Neil, S., Ben-Dov, E., Jones, A.F., Murphy, L., Quail, M.A., Holden, M.T., Harris, D., Zaritsky, A. and Parkhill, J.		
		TITLE	Complete Sequence and Organization of pBtoxis, the Toxin-Coding Plasmid of <i>Bacillus thuringiensis</i> subsp. <i>israelensis</i>		
		JOURNAL	Appl. Environ. Microbiol. 68 (10), 5092-5095 (2002)		

FEATURES	source	CDS
PUBMED REFERENCE AUTHORS TITLE JOURNAL COMMENT	PARKHILL J. Direct Submission Submitted (19-APR-2002) Submitted on behalf of the pBroxis sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk Notes: Details of pBroxis sequencing at the Sanger Centre are available on the World Wide Web. (URL, http://www.sanger.ac.uk/Projects/B_thuringiensis/).	
repeat_unit	1 . 121923 /organism="bacillus thuringiensis serovar israelensis" /mol_type="genomic DNA" /db_xref="taxon:1430" /note="plasmid pBroxis" 1.145 . 1.149 1.163 . 1.169 CDS /gene="pBroxis01" 1.163 . 1.2089 /gene="pBroxis01" /note="Similar in part to Bacillus anthracis pxol-49 TR:Q9XK19 (EMBL:AP065104) (227 aa) fasta scores: E(): 8.9e-44, 78.48% id in 158 aa" /codon_start=1 /transl_table=11 /protein_id="CAD30064_1" /db_xref="GI:21685411" /db_xref="UniProt/TREMBL:QBKNX5" /translation="MSTHLNFQNPKVGVKFDDGLENIIRKLENERKELPSALTYIMLHFECNDIGMLPREFOIMDAKKSGIPYTLYTGTQVCLERKLYTREIPIGNRTYEFIDALINHTAEEATDINISYSPYIQLQTLLKARDNGIMLLEJLNTFORKIGHYHKRICKDEPTIRNAFLKEBLNNAKVRQYEVKPKIFNAWDLDKKSESRSITRVRRQVQVIEKPNVIESNCVINDKCELHRPPAKCRIEAVSRKLKGQALLKKDNENIAFRQEVIDIEYLPLPKQKQN"	
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misc_feature	2.538 . 2.533 /gene="pBroxis03" /note="pBroxis hit to PF00665, Integrase core domain" 3.090 . 3.106 /note="IS240" /rpt_type=INVERTED 3.521 . 3.521 /note="UniProt/TREMBL:Q8KXN2" /rpt_type=INVERTED 3.612 . 4.319 /note="Similar to Bacillus thuringiensis insertion element IS240-a protein TR:Q45766 (EMBL:M23740) (235 aa) fasta scores: E(): 3.5e-91, 99.14% id in 235 aa, and to Mycobacterium fortuitum, transposase tnpa or tnp6100 TR:Q49185 (EMBL:X53635) (254 aa) fasta scores: E(): 1.1e-37, 48.05% id in 231 aa" /codon_start=1 /transl_table=11 /product="insertion element IS240 protein" /protein_id="CAD30066_1" /db_xref="GI:21685413" /db_xref="UniProt/TREMBL:QBKNX5" /translation="MEKENIIFKWKHYQADMILATWVRLRNLSFRDLVEMMERGLSLSHTRIMRWVHOYGPELNERIKHLKRKRTNDWRVDTYIKKGEMNYLYRAVDSEGNTLDFYLISKRDAAKCFKLKALASFHVTKPRVITDGKNAKPVAIRELKNEESLPYGMPLRVKYLNMMIEODHRFIKKRLANLGIKSMQTAVNMIAGIZAMHMYTKGGQLKRAQSAQONQRCHIOLGLTA"	
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repeat_unit	RBS gene CDS /note="Similar to Bacillus anthracis pxol-17 TR:Q9XK28 complement (47 aa) fasta scores: E(): 2.1e-12, 68.08% id in 47 aa" /codon_start=1 /transl_table=11 /product="putative integral membrane protein" /protein_id="CAD30068_1" /db_xref="GI:21685415" /db_xref="UniProt/TREMBL:Q8KXN2" /translation="MAVLKDSNYIEMNTYNEIGFPKGIFWGLIFVVFMSIMIATFINLCK"	
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<i>/note="1 probable transmembrane helix predicted for pBc006 by TMHMM2.0"</i>		
RBS gene complement (5515..5519) complement (6451..8160)		
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complement (8168..8173)		
RBS	8947..8951	
RBS	8959..10653	
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Quy	499 TATAAACCGTATTACTACCTATTATGCCGTAATGAAATTATTATA 558	
Db	95925 TATAAACATACATACATTATCATGTATTAGCAACATTAGCTGCTTATA 95866	
Quy	559 CAACAGCTGCTGAATTGGCTATGAACTGAGATAACATCCTCAAGAAATTGAA 618	
Db	95865 AATCAAEGCTGAATTGGCTTGAAGGTATTAAACATCAGCAACAGCAAACTTAA 95806	
Quy	619 CCTAATGCTGGAAACATCAGATGACTATTAAACCTTTAAAGAAAATTACCTTAATAT 678	
Db	95805 CCTTGGCC--AACGAAATTGATTATCCGTAATGAAAGTATAGAAGATTAC 95749	
Quy	679 ATGAACTATTGTCGAATACCTATAGCAAGGACTAAATAACTTCGAAACGAACTTAA 738	
Db	95748 ACTTAATGCTGCTAACACTTAAACGCTTGAACATTAAAGGTTAAATTAAAACGCGCTGTAT 95689	
Quy	739 ATGAGATGGATATTAAATGATTATGAAAGTATGACTTAACTGTTAGATACT 798	
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Quy	799 ATGGCTCAATTTCCTTTTATGATATAAAAGAGATAACAGATTCAATAGGAGAAATGGT 858	
Db	95628 ACTGCTGTATTAGCTCTGTGACTCTTCCTPAATTAGTGTAGTAAATCCAAATA 95569	
Quy	859 GGATTAAACCTGAACTTACAGAGAAATTATAACAATCTGAAATAAATTGACCGCTCT 918	
Db	95568 GGTGTCCTAACATGCTACATTACTCGTAAATTCTGGCTTAACTGGTCTTA 95516	
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ORIGIN		
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Best Local Similarity 70.2%; Pred. No. 6.2e-18; Gaps 2;		
Matches 302; Conservative 0; Mismatches 122; Indels 6; Gaps 2;		
Qy 1659 AACTCTTAATTCTACACAACTTATTACATAGACTCGATACTGCTAACAAATGGCTGG 1718		
Db 3 ATCACTCAATTCTCACACAACTCGATTTTAAAGATTGCTTCAAATGGAACCGC 62		
Qy 1719 AAATACTCTCCATTATCTCTCATACATACCAAGGAACTATAGAAATAACACCTCAACG 1778		
Db 63 AAATACTCGAGCTGTATACTCTAGATTCCTAGATCCAGGG--TAGCAGAACCTGGTATGCC 119		
Qy 1779 ACTCAACACACACTTTCTGGTACAATTATAATTACATACCAAGGATTTCGGTA 1838		
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Db 180 CTAGAAATTCTCTAACGAGCTGAATTCTGCCTCAAATGAAACATATCTCTGTGTTAA 239		
Qy 1899 TCGTGAGATGTT---CAAACTCAATTATGATAAAATTGATAATTATACCAAT 1955		
Db 240 TCGTCGGBGTGTATATCACACACAGTACTATGATAAAATGAAATTCTGCCAT 299		
Qy 1956 TACTCCCTGTAGCCAAATAGAGAAACAAAATTAGAAACACTCACAAATAAT 2015		
Db 300 TACTCGTTATAGAGGGATAGAGAAACAAAATTAGAAACAGTACACAAATAAT 359		
Qy 2016 AAATACATTCTCAAATCTACACAAATAATCTTTAAATAGAAACGCAAACTATGA 2075		
Db 360 TAATACATTCTCAAATCTACACAAATAACCTTACATGAACTTACAGATTGA 419		
Qy 2076 TATGTTAA 2085		
Db 420 CATAGATCA 429		
RESULT 12		
AF285775 AF285775 4959 bp DNA linear BCT 16-AUG-2000		
LOCUS Bacillus thuringiensis subsp. finitimus parasporal inclusion		
DEFINITION Protein Cry (cry) gene, complete cds.		
ACCESSION AF285775		
VERSION AF285775.1 GI:9828609		
KEYWORDS		
SOURCE		
ORGANISM Bacillus thuringiensis serovar finitimus		
Bacteria; Firmicutes; Bacillales; Bacilli; Bacillus; Bacillus cereus group.		
REFERENCE 1. (bases 1 to 4959)		
AUTHORS Moore, G.D. and Debro, L.H.		
TITLE Cloning and Analysis of a Gene for Exosporium Enclosed Cry Protein		
OF Bacillus thuringiensis subspesies finitimus		
JOURNAL Unpublished		
REFERENCE 2 (bases 1 to 4959)		
AUTHORS Moore, G.D. and Debro, L.H.		
TITLE Direct Submission		
JOURNAL Submitted (07-JUL-2000) Biology, Jacksonville State University, 700 N. Pelham Road, Jacksonville, AL 36265, USA		
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Db 1556 CGCTCAATTCTCAATTCTAAAGCAATTCTCAACTTCAACTTCAAGCTATGACACATT 1615		
Qy 510 ATTACTACCTATTATGCCAAGCTAAATTCTAAATTACACAACTGCAG 1531		
Db 1472 AACGTATTATGAAAGCTTAAATGTTGAAATCTCGCTCCGGTCTCTGATCCAGAGGA 212		
Qy 390 ATTACACCATTCTACAGCTTACACAAAGCTTAAATGAACTTCAAC 449		
Db 1352 AGATCAGAAATAATTGGTCAAAATTGAAACCGGAAAGAACCTTTAAATCAAC 1411		
Qy 270 GTTAACAGAAANGCATAAACGCTAAAGTACAAACTTTAGAGGATTAGCAAAATT 329		
Db 1412 AATTCTACAGCTGTAAAGAAATAGCATTAGCTCTATGTTAAAGATGTATT 1471		
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Db 1556 CGCTCAATTCTCAATTCTAAAGCAATTCTCAACTTCAACTTCAAGCTATGACACATT 1615		
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Db 1676 AACATCAGGATCATGGATCAACCATCACCATTCACTTCAAGCTTCACT 1726		
Qy 630 AACATCAGATGACTATAACCTTTAAAGAAATAACCTTCAACTTAAACAGCT 509		
Db 1727 GNCATCAGGATCTTATGAGGCTTATGAGGCTTATGAAAGTATATAATTATTG 1786		
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ORIGIN

Query Match 8.7%; Score 180.4; DB 1; Length 3752;
Best Local Similarity 49.6%; Prod. No. 2.7e-15;
Matches 766; Conservative 0; Mismatches 706; Indels 72; Gaps 9;

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Db	647	AAAGGGGGCCGATATGGAGTATGGAGTATGGAGTATGGTC-----TATAT	700	Db	1460	TTA-----AAATGATATATTTCGAACTTTCGAGTAACTGTTACATGAAAT	1501
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Qy	680	GTAACATTATGTCGAAATCACTATAGAGGAGCTAAATAAACCTGAAAACCTTAATA	739	Qy	1520	CAGATAAAATAATTAAATGATGCCGCAATCAAGSTAACAGTCCTGTATAACAAACTCTA	1579
Db	761	CTAAATTATGGCTGCAAAACATATAGAAACAGTTAAATATGGAAACACCAATA	820	Db	1562	TTCACAAATAGAAATTACRAAATTCCTGTAAAGCTTGGAAATCTAGGATTC	1621
Qy	740	TGAGATGGTAGATTATGGATTATGGAGATAATGACTTACTGTTAGATCTA	799	Qy	1580	AGGTAATTGAGGACCTGGTACATAGGAGAAACTGGTTATTACAACTGCAAGGGC	1639
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Db	941	CTGAAAAATTATATGGCATATTCGTTTACACAACTTCAAAAGCTAG	1000	Db	1736	ATGCTTCAACTGTTTATGGATTTCTTAACTTACATCTTACATCAATTAC	1777
Qy	920	CITACCTGTAATTCAACCAAATCTCGTATATGGATAATTTACACGTTCAAGGCC	979	Qy	1760	TAGGAATACCACTCAGACTCAACACACTTTCTGTACAAATTATAATTTAC	1819
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AB193814				AB193814			
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DEFINITION				Bacillus thuringiensis			
Complete cds.				DEFINITION			
ACCESSION				ACCESSION			
VERSION				VERSION			
KEYWORDS				KEYWORDS			
SOURCE				SOURCE			
ORGANISM				ORGANISM			
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus				Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus			
cereus group.				cereus group.			
REFERENCE				REFERENCE			

AUTHORS	Ohgushi,A., Wasano,N., Saitoh,H. and Ohba,M.	Qy	596 ATATACATCCTCACAAATTGAAACCTAATGCTGGAACATCAGATGACTPATTATAAACCTT
TITLE	Identification and characterization of novel cry genes from an mosquito-specific <i>Bacillus thuringiensis</i> serovar sotto strain	Db	683 ATATAAATAGATCTATCTCCACTTTGGGT-----TCAAAGATATTATCATCT 736
JOURNAL	Unpublished	Qy	656 TAAGAGAAMATAPACTAAATAATAGTAACATGCAATACCTATGAGAGGACTAA 715
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AUTHORS	Ohgushi,A., Wasano,N., Saitoh,H. and Ohba,M.	Qy	716 ATAACITCGAAAAGAACCTAATAATGAGTGGACTATATTAATGATTATCGAGAGATA 775
TITLE	Direct Submission	Db	797 ATATCTCAAACAAAGATACTCCTGGTAGCTATAATAATCTGTAAGAGGAG 856
JOURNAL	Submitted (26-OCT-2004) Akira Ohgushi, Kyushu University, Graduate School of Agriculture, 6-10, Hakozaki, Higashi-ku, Fukuoka, Fukuoka, 812-8581, Japan (E-mail: ohgushi@obs.kyushu-u.ac.jp, Tel: 81-92-842-3028; Fax: 81-92-842-3028)	Qy	776 TGACTTAACTGTATAGTAACTATGGCTCAATTTCCTTTGATAAAGAGATA 835
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CDS		Qy	1016 ATACAAAATGAAAGTACGGAAATCGTTAGTGGTATTTGCAATGACTCTA 1075
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Db	563 ATCGCTCTTAAATACCTGAAATAACCTGCAATTCTCCTACACACTG 622	Qy	1655 GTGAACTCCCTAAATTCTACACAACTTATTAGCTGATCAGGCT 1714
Db	623 CCAATTGTTGATTTGATTTATCATCAAGGAGGGCTTATATGAGATGGAAAATG 682		

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OM nucleic - nucleic search, using bw model

Run on: February 15, 2006, 00:04:51 ; Search time 1255 Seconds
 (without alignments)
 11/072.418 Million cell updates/sec

Title: US-10-782-570-3

Perfect score: 2085

Sequence: 1 atgtgtcaaggaaatcacaca.....caaactatgatattgattaa 2085

Scoring table: IDENTITY_NUC Gapop 10_0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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ALIGNMENTS

RESULT 1
 ADR89398 standard; cDNA; 2085 BP.
 ID ADR89398
 XX
 AC ADR89398;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE AXMI-007 alternative start site coding sequence.
 XX
 KW ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
 KW expression cassette; transformation; transgenic; Plant; bacteria;
 KW lepidoptera; coleoptera; pest; pesticide; resistance;
 KW pesticidal activity.
 XX
 Bacillus thuringiensis.
 OS
 XX
 PH Key
 FT 1. .2085
 FT /*tag= a
 FT /product= "Alternative AXMI-007"
 FT

SUMMARIES

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	2	2085	100.0	2235	13	ADR89396	Adr89396 AXMI-007
	3	1794.4	86.1	2208	13	ADR89394	Adr89394 AXMI-006
	4	334.6	16.0	3940	1	AAN93054	Aan93054 Delta-end
	5	334.6	16.0	4571	1	AAN93059	Aan93059 Delta-end
	6	334.6	16.0	4934	1	AAN81490	Aan81490 Insectici
	7	331.4	15.9	3543	2	AAQ14669	Aaq14669 Dipteran
	8	331.4	15.9	3543	2	AAQ81178	Aaq81178 B.t. toxi
	9	161.2	7.7	4896	6	AAD43974	Aad43974 Bacillus
	10	161.2	7.7	4896	10	ADF31301	Adf31301 Bacillus
	11	161.2	7.7	4896	10	ADF31306	Adf31306 Bacillus
	12	158	7.6	2061	2	AAQ14670	Aaq14670 Dipteran
	13	158	7.6	2061	2	AAQ81180	Aaq81180 B.t. toxi
	14	148.2	7.1	3756	1	AAN50525	Aan50525 Bacillus
	15	101.7	5.6	15548	6	ABJ34155	Abj34155 Human imm
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	18	100.6	4.8	3535	1	AAN91003	Aan91003 Sequence
	19	100.6	4.8	3684	14	AEA61392	Aea61392 Bacillus

Page 2

Db	1681	TATTACATTAAGCTTCGATAGCTAACAAATTGGCTGAA-AATACTCTTCTTATATCTT	1740	DR	WPI; 2004-635574/61.
Qy	1741	CITACAATACCAGGATATTAGGAAATACCACCTAACAAAGCTTTCCTGTTCTGGT	1800	XX	P-PSDB; ADR9397.
Db	1741	CITACAATACCAGGATATTAGGAAATACCACCTAACAAAGCTTTCCTGTTCTGGT	1800	PT	New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids and polypeptides, useful for killing lepidopteran or coleopteran pests or for producing organisms with pesticide resistance.
Qy	1801	ACAATTATAATTAGAATAGGGAGTTTGGTATTCCAATTCAAGTACAGTA	1860	PT	XX
Db	1801	ACAATTATAATTAGAATAGGGAGTTTGGTATTCCAATTCAAGTACAGTA	1860	PS	Claim 1; SEQ ID NO 8; 178pp; English.
Db	1861	ACATTACCTTAANTCGAACATACCAATTATTTGAGATCTAACATCA	1920	XX	This sequence encodes an isolated delta-endotoxin. Some of the delta-endotoxin coding sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. The nucleic acid sequences of the invention are useful in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide resistance, specifically bacteria and plants. These proteins are useful for generating altered or improved delta-endotoxin or delta-endotoxin-associated proteins that have pesticidal activity, or for detecting the presence of delta-endotoxin or delta-endotoxin-associated proteins or nucleic acids in products or organisms.
Qy	1861	ACATTACCTTAANTCGAACATACCAATTATTTGAGATCTAACATCA	1920	CC	XX
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				Best Local Similarity	100.0%; Pred. No. 0;
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				Qy	61 ATTGCTGCACCTTAGTGCGGTTCTATTGTTGCTACTCTGTAGCCGTATAGCTGGG 120
				Db	211 ATTGCTGCACCTTAGTGCGGTTCTATTGTTGCTACTCTGTAGCCGTATAGCTGGG 270
				Qy	121 CTCACTTCTPATATCGGACCGATAGGAAATAATGGCTPATAATATCTTGTACC 180
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				Qy	511 AGAAATTAAAAGCTTACAGCTCTGGTACCTTACGCTTACGCTTACGCTTACGCT 570
				Db	421 GCCTTGACTCTTAATAATAGCTTACGTTGAGATGTTCAATGTTTATTCGAAATACCT 480
				Qy	571 GCCTTGACTCTTAATAATAGCTTACGTTGAGATGTTCAATGTTTATTCGAAATACCT 630
				Qy	481 GGTTTCCAACCTTAACGTTAAACTTAAACGCTTACGCTTACGCTTACGCTTACGCT 540
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				Qy	541 TTTCATTAAATTAAACGTTACACGTTAACAGCTTACGCTTACGCTTACGCTTACGCT 600
				Db	691 TTTCATTAAATTAAACGTTACACGTTAACAGCTTACGCTTACGCTTACGCTTACGCT 750
				Qy	601 CATCCTTCAAAATGAACTTAATGTTGAAACATGAGTACTATAAACCTTAA 660
				PI	Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;

XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT for producing organisms with pesticide resistance.

XX

PS SEQ ID NO 6; 178pp; English.

XX This sequence encodes an isolated delta-endotoxin. Some of the delta-endotoxin coding sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. The nucleic acid sequences of the invention are useful in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide resistance, specifically bacteria and plants. These organisms are useful for generating altered or improved delta-endotoxin, delta-endotoxin-associated proteins that have pesticidal activity, or for detecting the presence of delta-endotoxin or delta-endotoxin-associated proteins or nucleic acids in products or organisms.

XX Sequence 2208 BP; 842 A; 377 C; 308 G; 681 T; 0 U; 0 Other;

SQ Score 1794.4 ; DB 13 ; Length 2208;
Best Local Similarity 92.7% ; Pred. No. 3.9e-290 ;
Matches 198 ; Conservative 0 ; Mismatches 141 ; Indels 9 ; Gaps 2 ;

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QY 61 ATTGGCAGTTAGCGAGTACTATTTGATCCGGTAGCCGTATAGCTGG 120	Db 214 ATTGGCAGTTAGCGAGTACTATGGTATCCGGTAGCCGTATAGCTGG 273
QY 121 CTCACTTCTATATCGGACCGATGAAATAATAGTGCTATAATACTTTGGTAC 180	Db 274 CTCACTTCTATATCGGACCGATGAAATAATAGTGCTATAATACTTTGGTAC 333
QY 181 CTAATCACTGCTTTGGCCCGCGGGAGAACAGTATGGCACAATT 240	Db 334 CTAATCACTGCTTTGGCCCGCGGGAGAACAGTATGGCACAATT 393
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QY 421 GCCTTGACTCTAAATMCATTTGAGAAGTTTACAGTGTACCTTACAGTAAAGCT 480	Db 574 GCCTTGACTCTAAATMCATTTGAGAAGTTTACAGTGTACCTTACAGTAAAGCT 633
QY 481 GGTTTCACUTGAAACTATAAACGCTTAACTACCPATTATGCCGAGCTGTAA 540	Db 634 GGTTTCACUTGAAACTATAAACGCTTAACTACCPATTATGCCGAGCTGTAA 693
QY 541 TTTCATTAAATTAACTAACAGCTGCTGAAATTGGCTGTGAAATGGCTGTAA 600	Db 694 TTTCATTAAATTAACTAACAGCTGCTGAAATTGGCTGTGAAATGGCTGTAA 753
QY 601 CATCCCTCACAAATGACCTATTACAAAGCTGCTGAACTCGATGACTTAA 660	Db 754 CATCCCTCACAAATGACCTATTACAAAGCTGCTGAACTCGATGACTTAA 813
QY 661 GAAAATPACCTAAATATGTAACATTGTGCAAATACCTATAGGAACTGCTTAA 720	QY

Db 814 GAAAATPACCTAAATATGTAACATTGTGCAAATACCTATAGGAACTGCTTAA 873

Db 721 CCTCGAACAGAACCTAAATATGAGTGGATGATGTTGAGTATGACT 780

Db 874 CTTAGAGACGACCAAAATATGAAATGAGTGGATGATGACT 933

Db 781 ATTACTGTATTAGATACTATCCCTCAATTCTTGTATGATAGAGATAAAGAT 840

QY 934 ATTACTGTATTAGATACTATCCCTCAATTCTTGTATGATAAAGATAGAGAT 993

Db 841 TCAATAGGAAAGATAG-----GTGGCTTAAACTAACAGAAATTATPACA 894

Db 994 TCAATAGGAAAGATAGAGTAAAGGATTAGAAGTAAAGGAACTCACAGAGAAATTATPACA 1053

QY 895 ACTGAAATAAATTGACCGCTTACCTACCTGAATTCAACCAATCTCGTATATG 954

Db 1054 ACTGAATAAATTGATCGCTCTTCACCTAGGTCAACCAATCTAGTACGATG 1113

QY 955 GAATTAATTTAACCGTCAAGGCTTACGTTACCTGAATTTCGAACTTATATT 1014

Db 1114 GAATTAATTTAACCTGGCAAGTGTGTTAAATTCTTACGAACTTATTT 1173

QY 1015 TATCACAAAATGAACTAACGCTACCGGAATGTTGTAGTGTAAATGATCT 1074

Db 1174 TATACAGAAAATACAAATTTCGGGATCTGGTATGTTGTAGTGTAACT 1233

QY 1075 ACTTATGCTTACGACGAGACTGAAATTATGGAGAAAGACGGTCCACCAACAA 1134

Db 1234 ACTTATGCAATTACTATACTGAACTTATATGGAGAAAGACGGTCCACCAACAA 1293

QY 1135 AAACCTTAATACCTATGTAACCTTACCTAAAGTTCAATGTAAGTTCAATGTAAGTACT 1194

Db 1294 AAACACATAAGCCATTGAACTTATAAGTTCAATGTAAGTACATGACAACTACCT 1353

QY 1195 CCTACTTCCCCTTTCCPAACATATACCTTACATTAATCAAAATTGACTTTATTAAAT 1254

Db 1354 CCTGTTCCCTATT--AACACACATTAAATTCAATGAACTTTATTAAAT 1410

QY 1255 AACATACCTGTTACATTTAACATATTCAATTTCTGCGGAAATTCTPAATGATAAAA 1114

Db 1411 GGCTCATCTAACACACACTCAATATTCAAGGGGSGCTTCTATCTATTATCACAC 1470

QY 1315 ACACAGTATTCTTCAATTCTCTGTAATAAAAGACTGTAACCAATTATCAAAATGT 1374

Db 1471 ACACATTCTTCTGAAAAAAGACTGCACTCTAGTTATTGATCCAGGTTCT 1510

QY 1375 TTACCAAGCTTAAATAGTTAGCTATTTCCAGTTCTTATTAAATTATTC 1414

Db 1531 TCACCAAACCTTAAATRACTATGATGATTTTCAATTACTTATTC 1590

QY 1435 TATAAAATTGGTGTAGGGCTAAATTATGATGGTGTAACTGGTAACTGAGT 1494

Db 1591 TATGGTATTGGTGTAACTGCTTAAATTGATGGTGTAACTGGTAACTGAGT 1650

QY 1495 AGTGTAAATGAAATTATGCAATATCAGATAAAATTGATCCAGAAATCAA 1554

Db 1651 AGTGTGTGATGATGATTAATGCAATATCAGATAAAATTGATCCAGAAATCAA 1710

QY 1555 GTTACAGCTTGTGATACAAACTCTAAGGAACTGCTGTGATCATACGGGAAAC 1614

Db 1711 GTTACAACTTGTGATACAAACTCTAAGGAACTGCTGTGATCATACGGGAAAC 1770

QY 1615 TTGGTTTATTACAAAGTCAAGCTTGTGAAATGAGTTTACATGTAACACTCTCTAA 1674

Db 1771 TTGGTTTATTACAAAGTCAAGGGGTTGATGCTGAAATTACTCTCTTCTAA 1830

QY 1675 CAATTTTATTACATGAGCTTGTGAAATGAGTTTACATGTAACACTCTCTAA 1734

Db 1831 CAATTTTATTACATGAGCTTGTGAAATGAGTTTACATGTAACACTCTCTAA 1890

QY

Sequence Data from GenBank							
Db	2144	TATTTATTTTATTAAATGTCATAAGCTTAGATAATAATCTAAATGATTATAA	2203	XX	Insecticidal (Diptera) protein gene.		
Qy	1218	AFACTTCAATAATTAAATGGACTTTTAATTCACCTAGTATAAAATTCACCTA	1277	KW	Insecticidal protein gene; Diptera: Aedes; ss.		
Db	2204	TATATTAGTAAATGGATTTTTAACTAATGTTAACATTGTAAAGAAACT	2263	OS	Bacillus thuringiensis serovar israelensis.		
Qy	1278	ATATTCAAGCTGGGGAAATTCTAATGATAAAAACAACGATTTCAATTTCCTGT	1337	XX	Location/Qualifiers		
Db	2264	TACAGCAGCATGGCAAAATTAACTTATGTAATAAATGTTAACCTAACAT	2323	Key	1. 4908		
Qy	1338	AAAAGAACGTAAACCAATTATTAATCCAAATGTTAACAGCTATACTGTTAG	1397	CDS	/*:cg= a		
Db	2324	TCTTAACGAGAGAGAACTCAAGAAACCTTACCCCTTCCACATGATAACTATG	2383	FT	/product= "insecticidal protein"		
Qy	1398	TCAATTTATCCAGTTCITTTATTTAAATTCCPATAAAATTGGATTAGGGCTAA	1457	FT	620..1368		
Db	2384	TCTATTTTCAATTAAATGTTAAAGTCCTAGTATGCC-----TGAACTATA	2428	FT	/*:tag= b		
Qy	1458	TATTTATATACGGTGCATTAGATGGACACAGTAGTGTAAATGAAATGCAAT	1517	XX	PP	19-MAR-1987;	
Db	2429	TAAACTCTCAGTGTATACTGTTGGACACACTCTAGTGTATCCTAAATAACAT	2488	XX	PP	19-MAR-1987;	
Qy	1518	ATCGATAAAATATTACATATGTCACAGTCAACGTAACAGTCTGATCACACT	1577	PA	(SUMO) SUMITOMO CHEM IND KK.		
Db	2489	TTATACACATTAACTTAACTCCAAATTCCGCTAAAGCGAACTTCACCTGCTC	2548	XX	DR	WPI: 1988_311968/44.	
Qy	1578	TAAGGTTAATTGAGGACCTGTGTCATAACGGGAAACTTGTGTTATTACAACTCAAG	1637	XX	P-PSB; AAP81034 , AAP82559.		
Db	2549	TAGGGTTGTTAGGACCTGTGTCATAACGGGAAACTGGGGATTAAATGTTCAAAGATCA---	2605	XX	New insecticidal protein of bacillus tulingensis islaensis strain -		
Qy	1638	GGCTTATGAGGATTACATGTAAGACTCTTAATTCACAACTCTTATTACATTAGACTCTG	1697	XX	CC	Prep. by isolating plasmid contg. insecticidal protein gene by forming	
Db	2606	--TTCTCAAATTACATCTCAACACTTCAACATCGATTTTAACATCGATTTCAGT	2662	XX	PT	gene library from plasmid deoxyribonucleic acid, etc.	
Qy	1698	ATACGTCACAAATGGTGTGGAAATACTCTCTTACATAACAGGGAT	1757	XX	PT	Disclosure; Page ?; 9pp; Japanese.	
Db	2663	TTATGCTTCAAATGGAAAGCGCAAAATCTGAGCTGTATAAACCTTGTAGTCCAGGGGT	2722	XX	PT	A plasmid contg. the gene is isolated by forming a gene library from	
Qy	1758	ATAGGGATAACCCTCAACGACTCAACAACTTTCCTGTCATAAAATTATAAATT	1817	XX	CC	plasmid DNA of B.thuringiensis israelensis (HD 522 strain, USA Goldberg ONR0) followed by screening with anti-israelensis insecticidal protein	
Db	2723	AGCGAACTG--GGTATGGCACTCAACCCACATTCTGGTGTACAGATTATGAAATT	2779	XX	CC	IG. The insecticidal protein is highly effective against Diptera, esp.	
Qy	1818	ACATACGGGAAATTGGTATTCTCCATTCAAGTACAGTAACTTACCTTTAATTCTG	1877	Qy	CC	Diptera, esp. Aedes. (Updated on 24-Oct-2003 to standardise OS Field)	
Db	2780	AAAATATAAAGATTTCAGTACTTACGTTACGTTAACATCGATTTCAGT	2839	Db	CC	Sequence 4934 BP; 1797 A; 749 C; 877 G; 1511 T; 0 U; 0 Other;	
Qy	1878	AAACATACCAATTATAATTATGTCAGATGTT---CAAACTCAATTTCATCTGA	1934	Qy	PS	Query Match 16 0%; Score 334 6; DB 1; Length 4934;	
Db	2840	AAACATATCTCTGTGTTATCGTTGGATPATACACAGTACTTTATGAG	2899	Db	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Qy	1935	TAAAATGAAATTATACCAATTACTCTCTGACGCCAAATAAGAGAAAACAAATT	1994	Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Db	2900	TTAAAATGAAATTCTGCAAAATCTGTTAGGATAGAGAAACAAATTAAATT	2959	Db	Query Match 499 99%; Score 334 6; DB 1; Length 4934;		
Qy	1995	AGAAACTATCCAACAAATTAAATACATTTCTACAAATCATACAAAAATCTTAA	2054	Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Db	2960	AGAAACAGTACAAACAAATTAAATACATTATGCAAAATCCPATAAAACCTTACA	3019	Db	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Qy	2055	TATAGAAGCCAAACATGATGATTGATAA	2085	Qy	Query Match 559 99%; Score 334 6; DB 1; Length 4934;		
Db	3020	ATCGAACTTACAGATPATGACATAGATCA	3050	Db	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Qy				Db	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Db				Qy	Query Match 1972 99%; Score 334 6; DB 1; Length 4934;		
Qy				Db	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Db				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Qy				Db	Query Match 679 99%; Score 334 6; DB 1; Length 4934;		
Db				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Qy				Db	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Db				Qy	Query Match 2032 99%; Score 334 6; DB 1; Length 4934;		
Qy				Db	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Db				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Qy				Db	Query Match 2149 99%; Score 334 6; DB 1; Length 4934;		
Db				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Qy				Db	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Db				Qy	Query Match 2092 99%; Score 334 6; DB 1; Length 4934;		
Qy				Db	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Db				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Qy				Db	Query Match 2092 99%; Score 334 6; DB 1; Length 4934;		
Db				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Qy				Db	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Qy				Qy	Query Match 2209 99%; Score 334 6; DB 1; Length 4934;		
Db				Db	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Qy				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Db				Qy	Query Match 2269 99%; Score 334 6; DB 1; Length 4934;		
Qy				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Db				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Qy				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Db				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Qy				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Db				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Qy				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Db				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Qy				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Db				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Qy				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Db				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Qy				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Db				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Qy				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Db				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Qy				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Db				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Qy				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Db				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Qy				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Db				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Qy				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Db				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Qy				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Db				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Qy				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Db				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Qy				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Db				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Qy				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Db				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Qy				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Db				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Qy				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Db				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Qy				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Db				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Qy				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Db				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Qy				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Db				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Qy				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Db				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Qy				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Db				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Qy				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Db				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Qy				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Db				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Qy				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Db				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Qy				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Db				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Qy				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Db				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Qy				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Db				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Qy				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Db				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Qy				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Db				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Qy				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Db				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Qy				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Db				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Qy				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Db				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Qy				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Db				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Qy				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Db				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Qy				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Db				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Qy				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Db				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Qy				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Db				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Qy				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Db				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Qy				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Db				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Qy				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Db				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Qy				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Db				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Qy				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Db				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Qy				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Db				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Qy				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Db				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Qy				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Db				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Qy				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Db				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Qy				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Db				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Qy				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Db				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Qy				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Db				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Qy				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Db				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Qy				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Db				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Qy				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Db				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Qy				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Db				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Qy				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Db				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Qy				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Db				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Qy				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Db				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Qy				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Db				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Qy				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		
Db				Qy	Query Match 2329 99%; Score 334 6; DB 1; Length 4934;		
Qy				Qy	Best Local Similarity 53.9%; Pred. No. 1.1e-46;		
Db				Qy	Mismatches 0; Mismatches 695; Indels 38; Gaps 7;		

2382	AAGCCCTATAAATTGACTTCAATTAAGGATTCACTACAGCTAGCCGA	2441	Db	3438 AGAAACAGTACACAAATAATTATACATTITATGCATAATCCTATAAAAACCTTACA 3497
979	CTTAGATTATTTCATTTTGATGAACTTATTTATAACAAAATGAAACGTAGCGG	1038	Qy	2055 TATAGAGCCAACATGATGATATTGATAA 2085
2442	TTTATTACTTGGTTGATTCGGTATGCGAACCTTAAGATCTACTT	1097	Db	3498 ATCAGACTTACAGATCATGACATGATCAA 3528
1039	ATGGTTTACTGGTATGCGAACCTTAAGATCTACTT	1097	Qy	AAQ14669 standard; DNA; 3543 BP.
2502	TTTTTCAACGCCATTATAATTGTTCAATCACACTGATAATATCCAAAATC	2561	Db	AAQ14669;
1098	AATTATATTGAGAAAGAACGGTCAACCAACAAACTTAATACTTGAATC	1157	Qy	XX
2562	TAGTGTGTTGAAATCACAGTAACTGATAAATTAATCTCTGGTGGCACAAA	2621	Db	27-AUG-2003 (revised)
1158	CATAAAGTTCAATGTAACGTAGACAGTAACCTCCPACTTCCCCTTTCCTAACAT	1217	Qy	DT 25-MAR-2003 (revised)
2622	TATTATATTGTTTAACTTAATCAATGTAACCTTAATTAATCTAACTGATTAA	2681	Db	04-FEB-1992 (first entry)
1218	ATACTTACATTAACTCAATGTAACCTTAATTAATCTACCTAGTAATAAAC	1277	Qy	XX
2682	TAATATTGAAATGATTTTATAACCTAATGTAACCTAGACATTTGGAAAGRACT	2741	Db	DE Diptera active toxin gene.
1278	ATATTCAGCTGGGGAAATTATCTATGATAAAGCTGTTCAATTTCCTGT	1337	Qy	XX
2742	TACACCGGATCTGGCCTAAATTAACCTATGATGTRATAAATATTTGGTTACCAAT	2801	Db	XX Insecticide; B.t; crystal; delta endotoxin; cryIVA; 68.
1338	AAAAAAAGACTGTAACCAATTATTAACTCCAAATTGTTTACCAAGGCTATAATAGTTAG	1397	Qy	OS Bacillus thuringiensis serovar morrisoni.
2802	TCTTAAACGAGAGAACTTCAAGGAAACCCFACCCCTTTCCACATGATAACTATAG	2861	Db	XX
1398	TCATATTAACTCCAGTTCTTTATTAAATTCCTATAAATTCGATTGGCTTAA	1457	Qy	XX
2862	TCATATTATCATTATTAAAGTCCTATGATCC-----TGCAACATA	2906	Db	09-MAY-1991; 91EP-00304180.
1458	TATATTATATTAGGTGCAATAGGTAGTGTGACACACTGTGATCTAGTGTGATCTAAATAACAT	1517	Qy	XX
2907	TAACATCAAGTGTATACTGTGACACACTGTGATCTAGTGTGATCTAAATAACAT	2966	Db	15-MAY-1990; 90US-00524255.
1518	ATCAGATAAAATAATTACAATGATCCGAATCAAGGTACAGTCTTGATACAACTC	1577	Qy	XX
2967	TTATACATTTAACTACCCAAATTCCAGCTTAAAGCTGAAATTCAAGTCAAGG	1637	Db	01-OCT-1990; 90US-00590903.
1578	TAAGGTATTGAGGACTGTGCTATACAGGAAACTTCCAGTAAATGCTGTC	3026	Qy	XX
3027	TAAGGTGTTCAAGGCTGTCAAGGACTGTCAAGGAGGATTAAATGATTGATCAAGATCA---	3083	Db	PA (MYCO) MYCOGEN CORP.
1638	GGGTATTAGAGTAACTGTGAACTCTTCAACATTACATAGACTGCTG	1697	Qy	XX
3084	--TTTCAAAATTACATGCAACACTCAAATTTCACATGTTTAAATGATTG	3140	Db	WPI: 1991-341902/47. P:PSDAB; AARI373.
1698	ATACGCTAACAAATGGTGTGGAAATAACTCTCTCTTAATATCTCTACATACAGGACT	1757	Qy	XX
3141	TTATGCTCAATGGAACGCAAAATCTGACGTGTATAATCTCAGGCT	3200	Db	Bacillus thuringiensis genes encoding diptera-active toxins - and PT transformed microbes used to control insects in various environments.
1758	ATAGGDATAACCCTAACGACTAACACACTTCTGTTGACAAATTATAAATT	1817	Qy	XX
3201	ACGAGAACTG -- GGTATGGCACTCRACTCCACTTCTGTPACAGTATACGAATT	3257	Db	PI Sick AJ; XX
1818	ACRATACGAGATTTCGGTATTCTCAATTCCAGTACATGAACTTAAATG	1877	Qy	XX
3258	AAATAATAAGATTTCAGATTCACTGAAATTCTACGTTGAAATTGCTCAAATCA	3317	Db	XX
1878	AAACATACCTTATATTAACTGTCGAGATGTAT--CAAACTCAATTTCATCATCA	1934	Qy	WPT: 1991-341902/47. DR: PS71M3-69.
3318	AAACATATCTCTGTTAATCTCGTGTATATGCTGAACTTACATCTGACTGTATA	3377	Db	CC The sequence was obt. from plasmid pMYC1625 which was isolated from a genomic library prep. from DNA from B.t. PS71M3-69 (NRRL B-18515). It is related to the cryIVB family of genes, the 140 kD endotoxin gene and the type II gene from B.t. var. israelensis. The gene encodes a 130 kD protein. Microorganisms transformed with the DNA may be administered to dipteran insects or their environments, the expressed toxins acting as an insecticide. See also AAQ14670-014572. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 27-AUG-2003 to correct OS field.)
1935	TAAAATGAAATTATACCAATTACTTCTCTGTTGAAATTGCTCAAATGAA	1994	Qy	XX
3378	TAAAATGAAATTCTGCAATTACTGTTGAAATTGCTCAAATGAAACAAATT	3437	Db	604 TATAAAACGCTTATTACCTTATTGCGAAGCTGCTTAATTTCATTAAATTATA
1995	AGAAACTACTCACAACAAATAATAACATACATTTCACAAATCATACATCA	2054	Qy	559 CAACAGGTCTGAAATTGGCTGATGAAATTGCTCCTCACAATGAA 618
			Qy	664 AATCAACGGCTGAAATTGCTGAAATTGCTGACATTGCTGATTTAGG 723
			Qy	619 CCTAAATCTGAAACATAGATGACTTATAAACTTAACTTAACTTAAAT

Db	724	CCCTTGCC---AACGGCAATTGATTATTCAGTATGACTAAAGCTTAAAGATTAC 780	Db	1773	TATGGCTCAAATGGAGCGCAAATACAGAGCTGTATAATCTTAGTATCCAGGG- 1831
Qy	679	AGTAACATTGTCAAATACCTATAGAAGGACTAAATTAACCTTCGAACGAACTTAAT 738	Qy	1758	AATAGGATAACCCCTAACGACTCAACAACACTTTCTGTACAAATTATAATTT 1817
Db	781	ACTTAATTTGTPACACTTAAAGGATTAAATTAAAGGATTAAATTAAAGCCTGAT 840	Db	1832	--TAGGAGAACCTGGPATGGCACTCAACCCCACCTTTCGSGTACAGTATAGGATT 1889
Qy	739	ATGAGATGGAGTATTTATGATTATGAAAGATATAATGACTTATGAGACT 798	Qy	1818	ACAATAGGGATTGGATTTCGAATTCGAAGTAACTTACCTTAAATCG 1877
Db	841	AGTAATCTGATGGAATAATTAACCTGGAAACCATACATACATACCTGGACTAACT 900	Db	1890	AAAATTAAGATTTOAGTACTTAAATGAGTTCTAAGGAGTGAATTGTCGATCA 1949
Qy	799	ATGGCTCAATTCTTCTTATGTTATGATAAGGATAACAAGATTCAATAGGAGAATAGT 858	Qy	1878	AAAATCACCATTATTTAAATCTGTCAGATGTT--CAAATTCAATTPTTAATCTATTGA 1934
Db	901	ACTGCTGTTATTAGATCTGTTGGACTCTTCTCTTAATTATGAGTAGTGTAACTGATA 960	Db	1950	AAACATPATCTCTGTTTTAATCTGTTGGATGTTATAACACAGTACTTATTGA 2009
Qy	859	GGCATTAAACTGAACTTAAAGGAAATTATAACAACTGAAATAATTGACCGNCT 918	Qy	1935	TAATATGAAATTACCAATTACTCTCTGTCAGATGTT--CAAATCAGGAAACAAATT 1994
Db	961	GGTGTCCCATCTGAACTTAACTCTGAGAAATTAT-----CGGTGACTTAACTTCGAAGA 1013	Db	2010	TAAAATGAAATTCTGCAATTACTGTTCTPATAAGAGGAGTAGGAGAAACAAATT 2069
Qy	919	ACTTACCTGAAATTCAACCCAAATCTGCCTTAATGGAAATAATTAAACGTTCAGG 978	Qy	1995	AGAAACTATCCAAACAAAATAATCATTTTCAAAATCATAACAAAAAAATCTTAA 2054
Db	1014	AACGCCCTATAAATATTAGCATTATGACGTTCAAGGTTACAGCTTAACTCTCTTAATAA 1133	Db	2070	AGARAGTGTACRCAATTAAATTAATGAAATTGAACTTATGAAACTTAACTTACA 2129
Qy	979	CITGAGTATTTCATTTTAGTGAACCTATATTITATACAAAAATGAAACGTCGG 1038	Qy	2055	TATGAAAGGCCAAACTATGATATTGATTAA 2085
Db	1074	TITATTTCATTGCTGCTGTTGATTCTTGTAAATTGAAATGAAAGGCAAAACTCTCTTAATAA 1133	Db	2130	ATCGGAACTTACAGATTATGACATAGATCAA 2160
RESULT 8					
		AAQ81178	AAQ81178	AAQ81178	AAQ81178
		ID	ID	ID	ID
		XX	XX	XX	XX
		AC	AC	AC	AC
		XX	XX	XX	XX
		DT	DT	DT	DT
		25-MAR-2003	(revised)	12-AUG-1995	(first entry)
		XX	XX	XX	XX
		DB	DB	DB	B.t. toxin PS71M3 gene.
		XX	XX	XX	Delta-endotoxin; crystal protein; biological control agent; Calliphoridae; insecticide;
		KW	KW	KW	screw-worm; sheep blowfly; lucilia; Phormia; pesticide; B.t.; 86.
		XX	XX	XX	Bacillus thuringiensis.
		OS	OS	OS	
		PN	PN	PN	W09502694-A2.
		XX	XX	XX	
		PD	PD	PD	26-JUN-1995.
		XX	XX	XX	
		PF	PF	PF	13-JUL-1994; 94WO-US007902.
		XX	XX	XX	
		PR	PR	PR	15-JUL-1993; 93US-00093199.
		XX	XX	XX	(MYCO) MYCOGEN CORP.
		PA	PA	PA	
		PI	PI	PI	Hickle LA, Payne J;
		XX	XX	XX	
		DR	DR	DR	WPI-1995-067138/09.
		DR	DR	DR	P-PSDB; AR63018.
		XX	XX	XX	
		Method for controlling Calliphoridae pests - specifically utilises Bacillus thuringiensis isolates or toxins.			
		PS	PS	PS	
		XX	XX	XX	
		CC	CC	CC	A library was constructed from <i>Bacillus thuringiensis</i> PS71M3 total cellular DNA in lambda Gem-11. Plasmid pMYC1625, selected in <i>Escherichia coli</i> , contained a 8.0 kb insert expressing a beta-endotoxin gene. This sequence (AAQ81178) is a cured, acrystalliferous B.t. host carrying pMYC1625 produced a 130 kDa crystal protein (AAR63078) toxic to calliphorids. (Updated on 25-MAR-2003 to correct PN field.)
		CC	CC	CC	
		XX	XX	XX	sequence 3543 BP; 1278 A; 566 C; 612 G; 1087 T; 0 U; 0 Other;
		SQ	SQ	SQ	

Query Match Best Local Matches	15.9%; Similarity 85%; Conservative	Score 331.4; DB 2; Length 3543;	Db	1599 TATACACATTAACTTCAAGGAAATTCAACTTGGAAGCTTC 1688
Qy 499	TATAAACCGCTATTACTA CCTATTATTCGCAAGCTGTAAATTATTAA	DB 53.8%; Prd: No. 3. 7e-46; 0; Mismatches 69; Indels 38; Gaps 7;	Qy	1578 TAAGGTTATTGAGGACTCTGGTCAATTAGGGAAACATTGCTTAAAGCAGTCAAGG 1637
Db 604	TATACACATTACTA CTATTACTA GTTCAACAGGAAACCTACATCGTACTGTTAA		Db	1659 TAAGGTTGTCAGGACTCTGGTCAATTAGGGAAACATTGCTTAAAGCAGTCAAGG 1715
Qy 559	CACAAAGGTGCTGAATTGCTGTAATGGAATGCAAGTATACATCCCTCACAAATGCA		Qy	1638 GCCTTATAGGATTACATGTAAGCTTAATCTACACATCTTAACTATAGACTTGC 1697
Db 664	AATCAAGCGCTCAATTGAGGTATTAAACATCGAACATTGCAATTGTTAGAG		Db	1716 --TTCTCAAATTACAGCTCAACACTCAAAATTCTCAGATCTTATAGAATTG 1772
Qy 619	CTTAATGCTGGAACTCATGACTTAAACCTTAAAGAAAATAACCTAAATAAT		Qy	1698 ATACGCTACAAATGGCTGGAATAATCTCTCTTCAATACATGGAGT 1757
Db 724	CCPTGCC --ARGAGCAATTGATTATTCCTGTTGACTAAAGCTTAAAGATTCAGATGATC		Db	1773 TTGCTCAAATGGAACTCATGTTAAATCTTAGTATCCAGGGG- 1831
Qy 679	AGTAACATTGTGCAAATACCTATAGAGGAGCTAAATAACTTCGAAACCTTAAT		Qy	1758 AATAGGAAATACCCTCAACGACTCAAGAACACTTCTCTGTCACAAATTATAATT 1817
Db 781	ACTAATTATGTGTAACACTTAAAGGATTAATTAACAAAGCAGCCGTAT		Db	1832 --TAGCAGAACTGGTATGGCACTCAACCCACTTCTCTGTCACAGTATACTGATT 1889
Qy 739	ATGAGATGGAGTATATTATGATTATGAGATATGACTTAACTGTTAGATACT		Qy	1818 ACATACGGAGATTGGTATTCCAACTTCAAGTAACTACCTTAAATCG 1877
Db 841	AGTAATCTGTGAAATTAAACTGGAAACATACATGGAAACATACATGGCTCT		Db	1890 AAATATAAGATTCTAGTACTTAACTGTTCTAAGCAGGTGAAATTGCTCCAATCA 1949
Qy 799	ATCGCTCAATTCTTTATGATAATAAGAGATAACAAGATTCAATAGGAAGTACCT		Qy	1878 AAACATACCTTATATTAACTTAACTGTCAGATGTAT--CAAATTCAATTAACTATGCA 1934
Db 901	ACTGCTGTTAGACTCTGTTGACTCTTCCTCTTCAATTAGTGTAGTAAATTCGATA		Db	1950 AAACATATCTCTGTTAACTGTCGATGTTAAACACAGTACTTATGCA 2009
Qy 859	GCGCTAAAACTGAACTTCAAGGAATTATAACATGAAATTTCGCTCT		Qy	1935 TAAATTGAATTATACCAATTACTCTCTGTCAGGCCAAATTAGGAAAAACAAATT 1994
Db 961	GGTGTCCCAATCTGAACTTACTCGAAATTATGAAATTATGAAATTATGAAATT		Db	2010 TAAATTGAAATTACTGTCGCAATTACTGTCGTTCTATAAGAGGATAGAGAAACAAATT 2069
Qy 919	ACTTACCTTGAATTCAACCCAACTCGGTATATGGGATAATTACAGTTCAAGG		Qy	1995 AGAAACTATCCAAACAAAAATAATACATTTCACATACAAANAACTTAAA 2054
Db 1014	AAGGCCCTTAATAATTATTAGTAACTTCAATATCGAAGGGTCACTTACGTAGACCCCA		Db	2070 AGAAACGTCAGTACAAATTATACATTATGCAATTCTPATAAAACACTTTACA 2129
Qy 979	CTTGGATTATTTCATTTTAGTGAACCTTATTTATAACAAAATGAACTACCGG		Qy	2055 TATAGAAGCCACAAACTATGATATTGATTGATTAA 2085
Db 1074	TTTATTACTCTGGTTGATCTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTG		Db	2130 ATCGAACTTACAGATTGACATGATGATCAA 2160
Qy 1039	AATCGTTAGTTGGTATTGCAATGTTAAAGATCTACTT-ATGATCTACT-		RESULT 9	
Db 1134	TTTTTTCACAGCCATTAAATGTTCAATTACATGTTAACTGATAATATCCAAAATC		ID AAD43974 standard; DNA; 4896 BP.	
Qy 1098	AATTTATATTGGAAGAACAGTCACCCACACATTAACTTACCATTTGAAAC		XX XX	
Db 1194	TAGCTTTTGGAAATCACATGTAACGTGATAATTAAATCTCTGTTGGCAACAAA		AC AAD43974;	
Qy 1158	CTATAAAAGTTCAATTGTAACTGTAGAACAGTAACCTCTACTTCCCTTTCTTAAC		DT 13-DEC-2002 (first entry)	
Db 1254	121.8 ATTCTTACATTAACTCAATTGAACTTAAATTCACCTGTAAATAATTAC		DB Bacillus thuringiensis ssp. finitimus cry2Ba1 gene.	
Qy 1218	121.8 ATTCTTACATTAACTCAATTGAACTTAAATTCACCTGTAAATAATTAC		KW Delta-endotoxin; cry2Ba1; insect-resistant plant; toxin;	
Db 1314	13.14 TAATTTAGTAAAATGTTTTTAACTAACTTAACTGTAACTGTTAGTAA		KW transgenic host cell; insecticide; gene; ds.	
Qy 1338	13.38 AAAAAGACTGTAAACCAATTAACTCAATTGAACTTAAATTCACCTGTAA		XX Bacillus thuringiensis.	
Db 1434	14.34 TCTTAACAGAGAAATCAAGGAAATTCAAGGAAATTCAAGGAAACT		XX Key	
Qy 1398	13.98 TCATATTATTCCTCAGTTCTTATTAAATTCTTAAATTCCTTAAAGCTT		XX 1129 -4458	
Db 1374	13.74 TACAGCGAGTCTGGCAAAATTAACTGTAACTGTTAGTAAATTTGGTT		FT FT	/tag= a
Qy 1494	14.94 TCATATTATTCATTAAAGTCATTGTTACCTTACCTTACCTTACCT		FT FT	/product= "cry2Ba1 gene"
Db 1458	14.58 TATATTATATCAGGGCAATTAGTGGCAACAGCTAGTTAAATGAAAT		XX US2002038005-A1.	
Db 1539	15.39 TAAACTCAATTGTAACTGTAACTGTAACTGTTGATCTCCTAA		XX 28-MAR-2002.	
Qy 1518	15.18 ATCAGATAAAATAATTACATGATCCAGCAATCAAAGTAAACGCTTC		XX 08-JAN-2001; 2001US-00756526.	
Db 1539	15.39 TAAACTCAATTGTAACTGTAACTGTAACTGTTGATCTCCTAA		XX 07-JAN-2000; 2000US-0175158P.	
Qy 1518	15.18 ATCAGATAAAATAATTACATGATCCAGCAATCAAAGTAAACGCTTC		XX (WOJC) WOJCIECHOWSKA J A.	
Db 1539	15.39 TAAACTCAATTGTAACTGTAACTGTAACTGTTGATCTCCTAA		XX (LEWI) LEWITIN E I.	
Qy 1518	15.18 ATCAGATAAAATAATTACATGATCCAGCAATCAAAGTAAACGCTTC		XX (ZALU) ZALUNIN I A.	
Db 1539	15.39 TAAACTCAATTGTAACTGTAACTGTAACTGTTGATCTCCTAA		XX (REV) REVINA L P.	
Qy 1518	15.18 ATCAGATAAAATAATTACATGATCCAGCAATCAAAGTAAACGCTTC		XX (CHESS) CHESTUKHINA G G.	

XX Wojciechowska JA, Lewitin EI, Zalunin IA, Revina LP;
 PI Chestukhina GG;
 XX WPI; 2002-403936/43.
 DR P-PSDB; AAE6353.

XX Novel isolated delta-endotoxin nucleic acid molecules, cry26Aa1 and cry28Aa1 isolated from *Bacillus thuringiensis* finitimus, that encodes toxin active against insects, useful for controlling insects.

XX Claim 1; Page 33-37; 42pp; English.

XX The invention relates to isolated delta-endotoxin nucleic acid molecules, cry26Aa1 and cry28Aa1 isolated from *Bacillus thuringiensis* finitimus, that encode a toxin that is active against insects. The invention is useful for producing an insect-resistant plant, by introducing the nucleic acid molecule into the plant, where the nucleic acid is expressible in the plant in an effective amount to control an insect. The invention is useful for producing a toxin that is active against insects by obtaining the transgenic host cell and expressing the nucleic acid molecule in the host cell, which results in the toxin that is active against insects. The toxin is useful for controlling an insect by delivering to the insect an effective amount of toxin. The invention is useful for controlling insects. The toxin is useful for inhibiting the ability of insect pest to survive, grow or reproduce, for limiting insect related damage or loss in crop plants, and to prophylactically treat insect susceptible areas or plants to confer protection or resistance against harmful insects. The present sequence is *Bacillus thuringiensis* spp. Finitimus cry28Aa1 gene

XX Sequence 4896 BP; 1727 A; 757 C; 887 G; 1525 T; 0 U; 0 Other;

XX Query Match Similarity 7.7%; Score 161.2; DB 6; Length 4896;
 Best Local Matches 385; Conservative 57.0%; Pred. No. 8.9e-18;
 XX Mismatches 243; Indels 48; Gaps 3;

XX Qy 153 AGGTGCCTATAATATCTTGGTACCCATACTCAGTCCTTTGGGCCGGAGAAC 212
 Db 1293 AGGTGTGTTACTATATCTTGGAACTTGCTCCGGTCTGGCTGATCCAGAGGA 1352
 XX Qy 213 AGA -- CAAACAGTATGGACACAATTATTAATGGGAGAAATTCTGTGATACAC 269
 Db 1353 AGATCCAAAAAAATTGGTACAATTATGGTACAATTTGAAACGGAGAACCTTAAATCAAC 1412
 XX Qy 270 GTTAACGAAAGGATAAAAGCTTAAGTGTACAACCTTAGAGGATTAGACAATAT 329
 Db 1413 AATTCTACAGCTGTAAAAGGAAATAGCATAGCTCATCAAATGGTTTAAAGATGAT 1472
 XX Qy 330 ACAAGCTATAATACGCTTACGATGATTGAGGAAATTAAAGACTAACAGCTCCGG 389
 Db 1473 AACGTAATGAAAGGATTAATGATTGGAGAGAAATCCAAGTGCAATACTGCCAG 1532
 XX Qy 390 ATTACCCACATCATCGCATTAACACAGCTGACTCTAAATACGATTGAGAA 449
 Db 1533 ATGGTATCACAGA-----GATTTGAA 1556
 XX Qy 450 TGTTCACATGATTATTCGAAATACTCTGGTCCACTGAACTTAAACGCT 509
 Db 1557 CGCTCATTCATTTGTAAGAAATGCAACTCCACACTTCCAGTGACACATT 1616
 XX Qy 510 ATTAATCCTATTATGCCAGCTGTTAACTTACATTAACAAAGCTGC 569
 Db 1617 ATTAAATGGTGTGATAGAGCTGAAATTACATGGATTACATCAGTGT 1676
 XX Qy 570 TGAATTGGCTGATGAAATGCAAGATACTACATCCTTCACAAATGAAACCTTAATGCTGG 629
 Db 1677 ACATTCGGTCAATGAACTGAACTTACCAACATTCACCAAT-----GTTGAA 1727
 XX Qy 630 AACATCAGTGAATTAATCTTAAAGAAAATATACCTTAATATACTAACTATGG 689
 Db 1728 GTCATCAGGTACTTATGACGAGCTPATGSTATAATGAACTTAACTATGG 1787
 XX SQ Sequence 4896 BP; 1727 A; 757 C; 887 G; 1525 T; 0 U; 0 Other;
 Best Local Similarity 7.7%; Score 161.2; DB 10; Length 4896;
 Pred. No. 8.9e-18;

XX RESULT 10
 ADP31301 ID ADP31301 standard; DNA; 4896 BP.
 XX AC ADP31301;
 XX DT 12-FEB-2004 (first entry)
 XX DB *Bacillus thuringiensis* serovar *finitimus* PF2 DNA clone.
 XX KW Cry26Aa1; cry28Aa1; delta-endotoxin; insect pest control; transgenic plant; insect resistance; insecticide; gene; ds.
 XX OS *Bacillus thuringiensis* serovar *finitimus*.
 XX Key PT CDS
 XX Location/Qualifiers
 PT / *tag= a
 PT /product= "Cry28Aa1 delta-endotoxin protein"
 XX FT XY
 XX PN US2003150018-A1.
 XX PD 07-AUG-2003.
 XX PP 15-JAN-2003; 2003US-00345020.
 XX PR 07-JAN-2000; 2000US-0175158P.
 XX PR 08-JAN-2001; 2001US-00756526.
 XX PA (WOJCIECHOWSKA J A.
 PA (LEWITIN E I.
 PA (ZALUNIN I A.
 PA (REVINA L P.
 PA (CHESTUKHINA G C.
 XX PI Wojechowska JA, Lewitin EI, Zalunin IA, Revina LP,
 PI Chestukhina GG;
 XX DR WPI; 2003-897633/82.
 XX DR P-PSDB; ADP31302.
 XX PT New isolated nucleic acid molecule encoding a toxin that is active against insects useful for controlling insect pests or for conferring insect resistance in plants.
 XX PT Claim 7; SEQ ID NO 3; 42pp; English.
 XX PS The present invention relates to the isolation of novel cry26Aa1 and cry28Aa1 delta-endotoxin genes from *Bacillus thuringiensis* spp. The sequences for the delta-endotoxin polypeptides are also disclosed. The invention provides methods for producing the toxins and compositions containing the toxins. The methods and sequences of the invention are useful for controlling insect pests in transgenic plants to confer insect resistance. The present sequence represents a DNA clone that contains the coding sequence for cry28Aa1 delta-endotoxin.
 XX SQ Sequence 4896 BP; 1727 A; 757 C; 887 G; 1525 T; 0 U; 0 Other;
 Best Local Similarity 57.0%; Pred. No. 8.9e-18;

Matches	385;	Conservative	0;	Mismatches	243;	Indels	48;	Gaps	3;	PD
DY	153	AGCTGCTATAATATATTGTTGACCCATACTGTCTTTGGCCGGAGACA	212	XX	14-AUG-2003.					
DY	1293	AGTGTGTTACTATCATTTGAACTTGCTCCGTCTTCGCTGATCAGAGGA	1352	XX	15-JAN-2003;	2003US-00342821.				
DY	213	AGA---CRAAACGATGACACAATTATTAAATGGAAATTTTGGTGTATACT	269	XX	07-JAN-2000;	2000US-0175158P.				
DY	1353	AGATCCAAAATATTGGTCATAATTGAAACGGAGACCTTAAATGCAAC	1412	XX	08-JAN-2001;	2001US-0175526.				
DY	270	GTTAACAGAAAGCATAAACAGCTTAAGTGTCAAACCTTGTAGAGGATT	329	XX	(WOJC/)	WOJciechowska J. A.				
DY	1413	AATTTCCTACAGCTGTAAAGGAAATAGCATATGGTTAAAGATGTAT	1472	XX	(LEWI/)	Lewitin E. I.				
DY	330	ACAAAGCTATAATACAGGTTAGTAGTGGAAATAAAGACTACAGCTCTGG	389	XX	(ZALU/)	Zalunin I. A.				
DY	1473	ATTACCACTCATCAGGATTACACAGAAATCCAACTGCAAAATACTGCAG	1532	XX	(REVIA/)	Revina L. P.				
DY	390	TGTTACATGATTATTGAGTGGAAATTTAAAGCTTAAATAGATTGGAA	449	XX	(CHESS/)	Chestukhina G. G.				
DY	1533	ATTGGTAACTACAGGCTTAATGGTCAATTAAGCTTAAATGGTAA	1556	XX	wojciechowska JA,	Lewitin EI,	Zalunin IA,	Revina LP;		
DY	450	TGTTACATGATTATTGAGTGGAAATTTAAAGCTTAAATAGATTAAAGCT	509	PS	wojciechowska J.A., Lewitin EI, Zalunin IA, Revina LP;					
DY	1557	CGTCATTCATTCAATTGTTGAACTGATATGCCACACTCCACAGTATGACAT	1616	XX	New delta-endotoxin nucleic acid molecules, cry26A1 and cry28A1, useful for controlling insect pests and for conferring insect resistance.					
DY	510	ATTACTACCTTATTGTTGCTTAATTGTTGAACTTAAATTGAAAGTG	569	CC	Claim 7; SEQ ID NO 3; 42pp; English.					
DY	1617	ATTATAAGTTGCTTACAGGCTGAAATTGATCAAGTGT	1676	CC	The present invention relates to the isolation of novel cry26A1 and cry28A1 delta-endotoxin genes from <i>Bacillus thuringiensis</i> spp. CC					
DY	570	TGAAATTGGCTGTGATGAAATGGAGATACTACATGAACTTGTG	629	CC	finitimus. The sequences for the delta-endotoxin polypeptides are also disclosed. The invention provides methods for producing the toxins and compositions containing the toxins. The methods and sequences of the CC					
DY	1677	ACATTGCGGATCAATGGAAATGGAACTTACATGAACTTGTGAA	1727	CC	compositions containing the toxins. The methods and sequences of the CC					
DY	630	AACTCAGATGACTTATTAAACCTTAAAGAAAATATACCTTAATAGTAACTATTG	689	CC	inventor are useful for controlling insect pests in transgenic plants to CC					
DY	1728	GTCATCAGGTTACTATTGAGCAGCTATTGGTATATGAAAGTATTATTG	1787	CC	conferr insect resistance. The present sequence represents a DNA Clone CC					
DY	690	TGCAAAATACCCATAGAGGGACTAAATAACTCTGAAAGAACCTTATATGGATGGAG	749	QY	Sequence 4896 BP; 1727 A; 757 C; 887 G; 1525 T; 0 U; 0 Other;					
DY	1788	CACCAAGACATAACCATAAAGGATGAACTTAAAGATCAGAAAATCATGGGA	1847	QY	Query Match 7.7%; Score 161.2; DB 10; Length 4896;					
DY	750	TATATTATGATTATGAGAGATAATGACTGATTAGATACTATCCCTCAATT	809	DB	Best Local Similarity 57.0%; Prod. No. 8.9e-18;					
DY	1848	TGCTTATAACATACATGCGAGAAATGACCTTAATTGATTGGATCTGTCGAACTT	1907	QY	Matches 385; Conservative 0; Mismatches 243;					
DY	810	TTCCTTTTGTGATA	825	DB	Indels 48; Gaps 3;					
DY	1908	TCCCTTTTGTGATA	1923	QY	Query Match 385;保守 0; 错配 243;					
DDB				DB	匹配 385; 保守 0; 错配 243;					
DY				QY	最佳局部相似度 57.0%; 序列号 8.9e-18;					
DDB				DB	匹配数 385; 保守 0; 错配 243;					
DY				QY	最佳局部相似度 57.0%; 序列号 8.9e-18;					
DDB				DB	匹配数 385; 保守 0; 错配 243;					
DY				QY	最佳局部相似度 57.0%; 序列号 8.9e-18;					
DDB				DB	匹配数 385; 保守 0; 错配 243;					
DY				QY	最佳局部相似度 57.0%; 序列号 8.9e-18;					
DDB				DB	匹配数 385; 保守 0; 错配 243;					
DY				QY	最佳局部相似度 57.0%; 序列号 8.9e-18;					
DDB				DB	匹配数 385; 保守 0; 错配 243;					
DY				QY	最佳局部相似度 57.0%; 序列号 8.9e-18;					
DDB				DB	匹配数 385; 保守 0; 错配 243;					
DY				QY	最佳局部相似度 57.0%; 序列号 8.9e-18;					
DDB				DB	匹配数 385; 保守 0; 错配 243;					
DY				QY	最佳局部相似度 57.0%; 序列号 8.9e-18;					
DDB				DB	匹配数 385; 保守 0; 错配 243;					
DY				QY	最佳局部相似度 57.0%; 序列号 8.9e-18;					
DDB				DB	匹配数 385; 保守 0; 错配 243;					
DY				QY	最佳局部相似度 57.0%; 序列号 8.9e-18;					
DDB				DB	匹配数 385; 保守 0; 错配 243;					
DY				QY	最佳局部相似度 57.0%; 序列号 8.9e-18;					
DDB				DB	匹配数 385; 保守 0; 错配 243;					
DY				QY	最佳局部相似度 57.0%; 序列号 8.9e-18;					
DDB				DB	匹配数 385; 保守 0; 错配 243;					
DY				QY	最佳局部相似度 57.0%; 序列号 8.9e-18;					
DDB				DB	匹配数 385; 保守 0; 错配 243;					
DY				QY	最佳局部相似度 57.0%; 序列号 8.9e-18;					
DDB				DB	匹配数 385; 保守 0; 错配 243;					
DY				QY	最佳局部相似度 57.0%; 序列号 8.9e-18;					
DDB				DB	匹配数 385; 保守 0; 错配 243;					
DY				QY	最佳局部相似度 57.0%; 序列号 8.9e-18;					
DDB				DB	匹配数 385; 保守 0; 错配 243;					
DY				QY	最佳局部相似度 57.0%; 序列号 8.9e-18;					
DDB				DB	匹配数 385; 保守 0; 错配 243;					
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DY				QY	最佳局部相似度 57.0%; 序列号 8.9e-18;			</		

		12-AUG-1995	(First entry)
Qy	1142 TAATACATTGAACTCCATAAAGTTCAACTTGTAACAGTACAAGTCTACTT	1201	XX
Db	1178 TTTCGAAGACATCCAAAGTATTCTTCTTATGAAACAAACCTATTGATAAGGTCG	1237	DE Delta-endotoxin; crystal protein; biological control agent; Calliphorid; KW scer-worm; sheep blowfly; Lucilla; Phormia; Calliphora; insecticide;
Qy	1202 CCCCTTTCCTACATACATACATACATACATACATACATACATACATACATAC	1261	KW pesticide; B.t. ss.
Db	1238 AAATTGTCAGACATAGAGTACTCAGATTAATATGAAAGTATTTTCGATA	1297	XX Bacillus thuringiensis.
Qy	1262 CTAGTAATAATTACATATTCACGTGGGGATTATCTTAATGATAAAAMAACACTG	1321	OS XX
Db	1298 GCAGTGAGTATTCGATATCATCCAAATTCAATTGAAATTATAAGACTG	1357	PN XX
Qy	1322 ATTTCATTCTCGTAAAAAAGACTGTAACCAATTATTAATCCAATTGTTACCA	1381	PD 26-JUN-1995.
Db	1358 ATTCCTATGATTCACAAACAAACATGAAATAAACATGAAATAACATGCT	1417	XX PP 13-JUL-1994; 94WO-US007902.
Qy	1382 GCTATAATGTTAGTCATATTATTCAGTCACTGAGCACACAGTAGTGTA	1441	XX PR 15-JUL-1993; 93US-00093199.
Db	1418 ATATATAACTGTAATTTATATTC	1445	XX XX
Qy	1442 TTGATTAGCGCTAAATATATACAGGTGCTTACAGTGCACACAGTAGTGTA	1501	PA (MYCO) MYCOGEN CORP .
Db	1446 -----AGTAGTAAAGAGAAGAGTGTAGTTGACACATACATAGTG	1498	PR Method for controlling Calliphoridae pests - specifically utilises Bacillus thuringiensis isolates or toxins.
Qy	1512 ATGAAATAATGCAATATGATAAAATTACATGATGCCAGCAATCAAAGTACA	1561	PI Hickie LA, Payne J;
Db	1499 ATTCACAAATAACATAGATTAGATAACATAGATTAGATAACATAGATT	1558	XX XX
Qy	1562 GTCTTGATAACAACTCTTCTGTAATTGAACTTGTGAACTTGTGTT	1621	DR WPI; 1995-067338/09.
Db	1559 AGGTAAAGTCTGTATTGAAATTGTGAAGTCTGTGAACTGGTGGACTTGTAA	1618	DR P-PSB; ARK63079.
Qy	1622 ATTACAAAGTCAGGGCTTTAGAGATTACATGTAACCTGAACTTGT	1681	XX DR
Db	1619 TTCTTAAAGATAGTATGGATTAGAGTTAGATTTAAAAAATGTTCTGCAAT	--	XX DR
Qy	1682 ATTACATTAGACTCTGATACTGCTACAATTGTCGTTGAAATTACATCTCC	1741	XX Sequence 2061 BP; 779 A; 331 C; 319 G; 632 T; 0 U; 0 Other;
Db	1676 ATCAGTACGTATTGCTATGCTACTCTCAAAAGAACAGTA-TTCTPAACCGG	1733	XX SQ
Qy	1742 TTCAAAATTGAACTCTAACCTCAAGCTCAACACTTTTCIGTA	1801	Query Match Score 158; DB 2; Length 2061;
Db	1734 AATAGATACTATAAGTGTGGACTTCCCTACTACCTTCCGCCAAAAAC	--	Best Local Similarity 48.3%; Pred. No. 3e-17;
Qy	1802 CAATTATAATTACATACAGGAGATTGGSTATTCACAACTTCCAAAGTACGT	--	Matches 99%; Conservative 0%; Mismatches 895%; Indels 174; Gaps 13
Db	1784 CAATGCTACAGATTAACTATGGAGATTGGATATGTAACATTCCAGAAACAGTC	1843	Qy 2 TGTGTCAGGGAAATACAGATAATGGTATAATTGCGACATTTGCTGATACAA 61
Qy	1860 -----ACATTACCTTAAATCCTAAACATACATTATATTATCTGGCAAGTGTAT	1912	Db 149 TGTGTCAGGGAAATACAGATAATGGTATAATTGCGACATTTGCTGAACTA 208
Db	1844 CAATAAAACATTGAAAGGGAAAGACACTTATTAATGACCTTATATGTAACCCAATC	1903	Qy 62 TTGCTGAGCTACTGCGCTACTATGGTACATTCGCGTACTATGGCTGATACAA 62
Qy	1913 CAAATTCAATTTCATTGATAAAATTGAAATTCTGTTGCTGC 1972		Db 209 TGTGTCAGGGAAATACAGATAATGGTATAATTGCGACATTTGCTGCCC 268
Db	1904 ATTCAATTATATATATGAAATTGAAATTCTGAAATTCTGATCTGATTAG	1963	Qy 122 TCACTCTATATCCGACCGATGAAATAATGGCTATAATATATCTGGTACCC 181
Qy	1973 AAAATAGAAAAACAAAAATTAGAAACACTTCACAAACAAATTTTCACAA	2032	Db 269 ----- CTGCTTCTGCTGGAGGTATATCTTGTGACCT 304
Db	1964 ATTATACAGGAAAGAAAAATGAGAAAAACAGAAAATGTTATTGTTA	2023	Qy 182 TAATCAGTCGTTGGCCGGGAAAGACAACAGTATGGACAAATTATTATA 241
Qy	2033 ATCATACAAAAAAATACTTAAATATAGA	2060	Db 305 TGTTGCGSATCTTTGGCAAGGGATCTGACCTG--.CAATGTTGGCGGATTTGTTAA 361
Db	2024 ATTAPACAAAGTTCTTACTAAATAGA	2051	Qy 242 AATGGGCAAAATTGGTGTGAACTTACAGCTTAAAGCTTAAAGGAAACAGCTAAAGTTAC 301
Qy			Db 362 ACATCGGGAAAGCTCTATACAGATAATTCAGCTTAACTTATGCTACTAATT 418
Db			Qy 302 AAACATTGAAAGGATTAGACAAATTATGAACTTACAGCTTAACTTATGCTACTAATT 475
Qy			Db 419 --.CTATGCTGACCTTAAATACACTGCTGATTTGCTGAAATTCTTGTAA 534
Db			Qy 362 GAAATTAAGGAACTACAGTCCTGGATTACCACTCATACAGCTTAACTGCTG 421
Qy			Db 476 GGAGGCCACGACGTACAGCTAAAGCTTAAGGCTA-CATGATCTCTTACTACCTTA 534
Qy			Qy 422 CCTGAGCTTAAATACATGTTGAAAGTGTGAAATTCTGAAATGTTACCTG 481

PS Disclosure; Page 15a-e; 27pp; English.	Qy 902 TAATTTGACCGCTTACTTACCTTGAAATTCACCCAAATCTGGCTATAATGGATAATA 961
XX CC The B. thuringiensis var. israelensis endotoxin insert in pSY367 is expressed in a bacterial host. The protein produced has insecticidal activity against dipteran insects. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)	Db 1902 -----ATTCAAGATACATTAGGCTTAACCTTGTGAAATGGCTATAATGGATAATA 1937
CC Sequence 3756 BP; Score 148.2; DB 1; Length 3756;	Qy 962 ATTAAACAGTTCAGGGTTAGATTATTCTGAACTTATTTAGATGAACCTTATTTATACAA 1021
CC Best Local Similarity 48.3%; Pred. No. 1..3e-15;	Db 1938 ATGGATAAATCTGAACTTACCTGAACTTACATTATTACTTGGATAAACBAGGGCTTTACCAA 1997
CC Matches 1001; Conservative 0; Mismatches 893; Indels 177; Gap# 14;	Qy 1022 AAAATGAAACGCTACGGGAAATCGTGTAGTGGTGTGATACA 61
XX Qy 2 TGTGTCAAACGGAAATACACAAATATGTCGAGCATTGCTTAGTGTGATACA 61	Db 1089 TGTGTCAAATACTAACTATGGCAATAATGGGAAATTGGCTAGGTCGAACTA 1148
SQ Db 62 TTGTGCAATTAGTGCAAGTCACTATTGTTTCGCGTACTCTGTGAGCCGTATAAGTGGGC 121	Qy 1142 TAATACCATTGATCCTATAAGTTCAATGTAACTGTAAGTAAGTAACTCTACTT 1201
Query Match 7.1%; Score 148.2; DB 1; Length 3756;	Db 1149 TTGTGCAATTAGTGCAAGTCACTATTGTTTCGCGTACTCTGTGAGCCGTATAAGTGGGC 1208
Best Local Similarity 48.3%; Pred. No. 1..3e-15;	Qy 2118 TTCTCAAGACACATCCAAAGATTTGATGAAACAAACTTATTGATAAGGTTGC 2177
Matches 1001; Conservative 0; Mismatches 893; Indels 177; Gap# 14;	Db 1202 CCCCTTTCCTAACATATACTTACAATTAACTTAACTTAAATTAATTCAC 1261
Qy 122 TCACTCTATATCGGACCGATAAGGAATAATAGTGTCTATAATATCTTGTGACCT 181	Db 2178 AATTGTCAGACATAGAGACTGACTGAGACTCTAGATAATGATAAAAAAAACACTG 12237
Db 1209 -----CTGTGTTAGTGTGAGGTATAATCTTGTGAGCT 1244	Qy 1262 CTAGTATAAATTAACATATTGAGCTGGGGAAATTPTCTATAATGATAAAAAAAACACTG 1321
Qy 182 TAACTCACTCTTGTGCCCGGGAGAACAGTGGACACAAATTATTA 241	Db 2238 GCAGTGGAGTATTGAGATTCTCACATTCACAACTTCACAAAGAAACTG 2297
Db 1245 TGTGCGGTCTCTTGGCAAGGATCTGCTG --CAATGTTGGCACTCTG 1301	Qy 1322 ATTTCAATTCTGTGAAAAGACTGTTAACCAATTATTAACTCAATTGTTACCA 1381
Qy 242 AAATGGGAAAATTTTGTGATACCCCTAACAGAAGCTAACAGCTAAAGTTCAC 301	Db 2298 ATTCCTATATGATTCTCACAAACAAACATGGAAATAATGAGAATAATGCTCATCTATCT 2357
Db 1302 ACATCGGGAAAGGCCCTATACAGAAATTAGATAAAAATTAATGTACTTACTT -- 1358	Qy 1382 GCTATAATGTCATATTTCATCCAGTTCTTTCTTTATTCTATAAA 1441
Qy 302 AAACTTAGGAGGTTAGACAAATTACAAAGCTTATAACAGCAATTAGTGGAA 361	Db 2358 ATATAAAACTGATAATTATATTTC----- 2385
Db 1359 ---CTATCGTAACCTATAAATACATTGTATAATTCGATAATTTCGATAAAAT 1415	Qy 1442 TTGGATTAGCGCTAAATATATTATACTAGGTGCTATTAGGATGGCTACAGGAAACTTGGTT 1501
Qy 362 GAAAATTAAAGAGCTACAGCTCTGGATTACCRCCATCATCGACATTACAACAGCTG 421	Db 2386 -----ACTAGTGAAGAGAGAAAGTGGCTATTAGTGGCAACATCTAGTGTG 2438
Db 1416 GGGACCCGGACGCTACACAGCTATGCTAACAGCTA 1474	Qy 1502 ATAGAAATAATGCAATTACGATAATAATTACATGATCCCAGCAATCAAGGTAACA 1561
Qy 422 CCTTGACTCTTAAATACGATTGAGAATTGCTTACATGTTATTGCGAAATACTCTG 481	Db 2439 ATTTCRCAAAATACGATATTGATGTTAGATACTACATCCACGCTCTAAACCTTTAA 2498
Db 1475 GAAACCTTAAATGATAAGGATTAGCTTAAATA 1511	Qy 1562 GTCTGATAACAACTCTAGGTAACTGAGGACTCTGGCTACAGGAAACTTGGTT 1621
Qy 482 GTTTCACCTGAAACTTAAAGCTTACCTATTATGCGAAGCTCTAATT 541	Db 2499 AGTGAATGCTTAATTCAAAATTCTGAAGGCTCTGTCACAGTGAAGACTTGGTA 2558
Db 1512 -----ATATGCTGAGCTTACGATCTGCAATGCAAAATAGCTACTT 1565	Qy 1622 ATTACAAGCTGAGGGCTTTAGAGATTACATCTGCTTAATTCTACACATCTT 1681
Qy 542 TTCACTTAATTATTACACAAAGGTGCTGATGATGGATGCAATATPC 601	Db 2559 TTCTTAAGATACTGAACTTAAATGAGTTAGAGTTAGAGTTAGAGTTAACTTCAACAA---T 2615
Db 1565 GGCACCTGAACTTAAACATGCTGAAATTCGAAATATCG 1625	Qy 1682 ATTACATTGACCTGATAGCTGAAACTTACCTTCCCTTAATATATCTC 1741
Qy 602 ATCCCTCACAAATGAACTTAATGCTGAACTGATGACTTATAACTTTAAAG 661	Db 2616 ATCAGTGTCTATGCTTATGCTACTAATGCTCCTAAAGCAACACT - -ATTCTCPAACCGG 2673
Db 1626 GT-----ATTAATCCAAAGPACTTCAATTCTCAATTACTATCAGGGCTATTAAAC 1679	Qy 1742 TTACDATAACGGGACTTAATAGGAAATTACACCTCAACGACTCAAACACACTTTCTGGTA 1801
Qy 662 AAAATATACCTAAATATGTAACCTATTGCTGAAATACCTTACCTTAAAC 721	Db 2674 AATAGATACTATAGTCTGGAGCTCTGTGACCTCTTCGGCAAAC-----C 2723
Db 1680 GTRAAATACGAAATACGATCTGACTTGTGATCTGCAATGCAAACTATGCA 1739	Qy 1802 CAATTTATAATTAATCTACATGCAATTCTGCTTATTCGAACTTCTGCTT 1859
Qy 722 TTGAAACGACCTTAATGAGATGGAGTATTAATGAGATGAAATATGACTA 781	Db 2724 CAAATGCTGAGATTAACTATGGAGATTGGATGATGAACTTTCAAGAACGTT 2783
Db 1740 TTAGACCTAAATACGAACTGAAATGTAATGTAATGCTGAAATGACTC 1799	Qy 1860 - -AATTTACCTTAAATGCAAAACTTACCTTATACTTCCGGCAAAC-----C 1909
Qy 782 TTACGTGTTAGTGTACTCTGCTCAATTCTTTTATGATAATAAGGATAACAAAGT 841	Db 2784 CAATTAACACTGCAAGGGRAAGCAGCTTTATTGTTGATGACCTTACCTGTCACCAA 2843
Db 1800 TAACGTGTTAGTGTACTCTGCTCAATTCTGAACTTACGCTAACTGCAAAATAA 1851	Qy 1910 TATCAAATGCAATTGTTAACTTGTGAAATTGAAATTTGAACTTACTCTCTGTAC 1969
Qy 842 CAATAGGAAAGATAATGCTGCAATTAAACTGACTAACAGAAATTATAACACTGAA 901	Db 2844 ATCATTCATATAATATATGCAAAATTGAAATTGAACTTACATCTGTAT 2903
Db 1852 -----TCCAAATGAGTTAAATCTGAACTTACGAGGTTACGAAATGTTACGAAATGTTA 1901	Qy 1970 GCCAAATGAGAAACAAACAAATTAGAAACACTATCCTAAACAAATAATACATTTC 2029

Db 12203 TATAAACATATATATACATATATATAACATATACTATAAATATAACTATAAAATAACA 12144
 Qy 1465 TATACAGGTGCATTAGGATGGCACACACTAGTGTAAATAGAAATATAGCAATATAGCAT 1524
 Db 12143 TATATATAACATATAAAATACATATAAAATACATATAAAATACATATAAAATACATATAAAA 12084
 Qy 1525 AAAATAATTACAAATGATCCCGAACATCAAGGTAAACGTCTGTATAACACTCTAAGGT 1584
 Db 12083 TAACATATAAAATACATATAAAATACATATAAAATACATATAAAATACATATAAAATAAT 12024
 Qy 1585 ATTGAAGGACCTGGTCATACAGGGAAACCTGGTTATTACAAAGTCAGGCGGTAA 1644
 Db 12023 AAAATAAAATATATAACATATAAAATACATATAAAATACATATAAAATACATATAAAATA 11964
 Qy 1645 GAGATTACATGTAGAACTCTTAATTCTAACAACTCTTACATTAGCTTCGATAACGCT 1704
 Db 11963 TATATAACATATAAAATACATATAAAATACATATAAAATACATATAAAATACATATAAAATA 11904
 Qy 1705 ACAATGGCTCTGGAATACTCTCTTAATATATCTCTAACATACCAACGAGTAATAGGA 1764
 Db 11903 ATAATATATAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 11844
 Qy 1765 ATACCACTAACGCTCACACACTTCTGGTACAAATATAATATTTAACATACATAC 1824
 Db 11843 TATAAAATATAAAATATAAAATATAAAATATAAAATATAAAATATAAAATATAAAATA 11784
 Qy 1825 GGAGATTTCGGTATTTCGAATTTCGAAGTAACCTTACCTTAATCGAAACATA 1884
 Db 11783 TAATATATAAAATATAAAATATAAAATATAAAATATAAAATATAAAATATAAAATATA 11724
 Qy 1885 CCATTATATTATTCGTCGAGATGTCAAATTCAATTCAATTCAATTCAATTGAA 1944
 Db 11723 AAAATAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 11664
 Qy 1945 TTATACCAATTACTCTCTGTAGGCCAAATAGAAAAACAAAAATTGAAACTATC 2004
 Db 11663 AAATATAAAATATAAAATATAAAATATAAAATATAAAATATAAAATATAATAATA 11604
 Qy 2005 CAAACAAATAATAATACATTTCACAAATCATACAAAAAAATACCTTTAAATATAGAAGCC 2064
 Db 11603 ATATATAAAATATAAAATATAAAATATAAAATATAAAATATAAAATATAATAATA 11544
 Qy 2065 ACAACTATGTATATGCA 2081
 Db 11543 ATAAATATAAAATA 11527

Search completed: February 15, 2006, 00:38:12
 Job time : 1272 secs

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Result No.	Score	Query Match	Length	DB ID	Description
c 1	100	4.8	2157	10 CL081966	CH216-165D13 Sp5.1 CH216 xenopus tropicalis genomic clone
c 2	98.4	4.7	1758	10 CL509408	CH216-165D13_ genomic survey sequence.
c 3	95.2	4.6	1981	10 CL082000	CH216-165D13_ genomic survey sequence.
c 4	90.2	4.3	1392	10 CG75703	GSS.
c 5	90	4.3	1539	10 AG340947	Xenopus tropicalis (western clawed frog)
c 6	90	4.3	1896	10 CG753093	Xenopus tropicalis
c 7	89.4	4.3	1542	10 AG386381	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
c 8	88.8	4.3	1608	10 CL118721	Xenopodinae; Xenopidae; Silurana.
c 9	88.4	4.2	1489	10 AG350139	REFERENCE 1 (bases 1 to 2157)
c 10	87.2	4.2	734	10 CNS010NP	AUTHORS Kremitski,C., Carter,J., McPherson,J., Warren,W., Graves,T., Mardis,E. and Wilson,R.
c 11	86.8	4.2	1348	10 CG749499	TITLE Unpublished (2003)
c 12	86	4.1	1101	10 AG386381	COMMENT A physical map of the xenopus tropicalis genome
c 13	85	4.1	1391	10 CG754863	JOURNAL Contact: Richard K Wilson
c 14	84.6	4.1	1242	10 CL068807	Washington University School of Medicine
c 15	84.6	4.1	2270	10 AG279277	Email: submissions@watson.wustl.edu
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					Best Local Similarity 43.6%; Pred. No. 2.5e-08;
					Matches 645; Conservative 0; Mismatches 820; Indels 13; Gaps 4;

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Qy	887 TTATACACTGAAATAATAATTGACCGTCTTACTTACCTTGAATTCAACCCAAATCTG 946
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SUMMARIES

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3	158	7.6	2061	3 US-09-224-024-30	Sequence 30, App1
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RESULT 1
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; Sequence 27, Application US/09224024
; Patent No. 605653
; GENERAL INFORMATION:
; APPLICANT: Leslie Hickle Payne
; TITLE OF INVENTION: Materials and Methods for the Control of
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,024
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/856,2226
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA79
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3543 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-224-024-27

ALIGNMENTS

Matches 856; Conservative 0; Mismatches 697; Indels 36; Gaps 7;

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RESULT 2
 PCT-US94-07902-27
 Sequence 27 Application PC/TUS9407902
 GENERAL INFORMATION:
 APPLICANT: Street address: 4980 Carroll Canyon Road
 APPLICANT: City: San Diego
 APPLICANT: State/Province: California
 APPLICANT: Country: US
 APPLICANT: Postal code/Zip: 92121
 APPLICANT: Phone number: (619) 453-8030
 APPLICANT: Telex number:
 TITLE OF INVENTION: Materials and Methods For the Control of
 TITLE OF INVENTION: Caliphorida Pests
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS: David R. Saliwanchik
 ADDRESSEES: STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: FL
 ZIP: 32606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/07902
 FILING DATE:
 CLASIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Saliwanchik, David R.
 REGISTRATION NUMBER: 31,794
 REFERENCE/DOCKET NUMBER: MA79

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 904-375-8100
 TELEFAX: 904-372-5800
 SEQUENCE FOR SEQ ID NO: 27;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3543 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 PCR-US94-07902-27

Query Match 15.9%; Score 331.4; DB 6; Length 3543;
 Best Local Similarity 53.8%; Pred. No. 3.3e-56;
 Matches 855; Conservative 0; Mismatches 697; Indels 38; Gaps 7;

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  Db 604 TATAATCATACTAGTATTATCTAGTTGCAAGAACCTACATGTATA 663
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  Qy 619 CCTAAATGCTGAAACATCGATGACTATTATAACCTTTAAAGAAAATACCTAAATT 678
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  Db 781 ACTAAATTATGTGAAACATTAAAGGTTAAATTAACGACCCTGT 840
  Qy 739 ATGAGATGGGTATTTATGATPATCGGAGATATGACTATTGATGATCT 798
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  Qy 799 ATCGCTCAATTTCCTTTATGATAAAAGGATAAAAGATTCAATAGGAAGGATAGGT 858
  Db 901 ACTGCTGTTAGCTGACTCTGCTTCTGATTTGAGTAAATCCCTA 960
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RESULT 3

US-09-224-024-30

Sequence 30, Application US/09224024

; Patent No. 6056953

; GENERAL INFORMATION:

; APPLICANT: Jewel Payne

; TITLE OF INVENTION: Materials and Methods for the Control of

; TITLE OF INVENTION: Calliphoridae Pests

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David R. Saliwanchik

; STREET: 2421 N.W. 41st Street, Suite A-1

; CITY: Gainesville, FL

; STATE: USA

; ZIP: 32606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/05/224,024
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: 08/856,226
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA79
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
SEQUENCE CHARACTERISTICS: 30;
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-09-224-30

Query Match 7.6%; Score 158; DB 3; Length 2061;
Best Local Similarity 48.3%; Pred. No. 4.3e-22;
Matches 999; Conservatve 0; Mismatches 894; Indels 174; Gaps 13;

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Qy	902	TAATTTGACCGCTTACCTTACCTSAATTCAACCCAAATTGGATAAAGGAAATA	961	Db	962	-----ATTCAGATACATTAGGATTAACGAACTGAACTGAA	997
Qy	962	ATTAACACGGTTAGGGCTTAACTTTCATTTTAGTAACTTATTTATACAA	1021	Db	998	ATGGATAAAGCTTACATTAACTGTTACCTTACGGAAACAAAGCTTACCAA	1057
Qy	1022	AAATGAAACGTCAGGGAAATCGTTAGTTGGTATGCTGAATGTTAGATCTACTPATG	1081	Db	1058	GAATTCCTGAGACATCTTCATCCCTTACGGTAACCAAGATGG 1117	
Qy	1082	CTACGAGGGAACTGAAATTATATGAGAAAGAAACGGTCACCCACAAACAAACTT	1141	Db	1118	CCTTCAACATACATAGTATGATGCAACATATCTGGGAGCGGTTCATGGACATTTA	1177
Qy	1142	TAATACCTTTGTAATCCTTAAAGTTCAATTGTAATGAGACAGTAACTCCCTACTT	1201	Db	1178	TTCTCTGAGACATCAAGATTCTCTTATGATTTATGAAACAAACACTTATGATAAGTGTG	1237
Qy	1202	CCCCTTTCTAACATATACTTTACATTTACATTAACTTAATCAATTGAACTTTAAATATTCAC	1261	Db	1238	AAATTGTCAGACATAGGAGTACTCGACATATAATGATAATGATGATTTCGAAATA	1297
Qy	1262	CTAGTAAATAATTAACTATTCAGCTGGGGAAATTATCTATGATAAAGAAACACTG	1321	Db	1298	GCAGTGAAGTATTCTGATATICATCCAACTCAATTAAATGAAATAATGAAAGACTG	1357
Qy	1322	ATTTCAATTCTCTGTTAAAGACTGTAACCAATTATTAATGATAATTGTTACAA	1381	Db	1358	ATCTATATGATTCTCCTACAAACATGGAAATAATGAAATAATGAAATGTTCTATGTTG	1417
Qy	1382	GCTATTAATAGTTAGTCTATTTTACGGTAAATTATGATAATTCTCTTAAATAAA	1441	Db	1418	ATATAAAAATGCTAAATGATAATTATGATAATTATGATAATTATGATAATTATG	1445
Qy	1442	TGGATTAATGGCTAAATATATATACGGTCACTAGGTTGATGTTGCTAAAGCTT	1501	Db	1446	-----AGTAGTTGAGAAAGGAGAGTGTGCAATTAGTGGACACATACTGTTG	1498
Qy	1502	ATAGAAATAATGCAATTATGAGATAAAATAATGAGTATCCGAAATCAAGGTAA	1561	Db	1499	ATTCCAAATACTACATGAGTTGAAATACATCCCAAATCAGCTTAAAGCTTGA	1558
Qy	1562	GTCCTGATAACACTCTAACGCTTAAGGAACTCTTACAGGAGGAAACTCTGTT	1621	Db	1559	AGGTAAGTCTGATGAAATGTTAAAGTGTAAAGCTGTTGAGACTGTTAA	1618
Qy	1622	ATTACAAAGTCAGGGCTTGTAGATTACATGAAACTCTTAATCTCACACACTT	1681	Db	1619	TCCTTAAGATAAGTGTGTTAAATGTTAAATGTTCTGCAAAAT--	1675
Qy	1682	ATTACATTAGCTTACGCTTACGCTTACGTTACATGTTGCTGAAATACTCTTC	1741	Db	1676	ATCAAGTACGTATTGTTATGCTACTATGCTCCAAAGAACAGGACTAACAC	1733
Qy	1742	TTACAAACCCCTAACACGAGTAATAGGAAATACCTATAGGAAATAAAC	1801	Qy	1742	-----	

RESULT 4
PCT-US94-07902-30
Sequence 30, Application PC/TUS9407902

GENERAL INFORMATION:

APPLICANT: Street address: 4980 Carroll Canyon Road
City: San Diego
State/Province: California
Country: US

APPLICANT: Postal code/Zip: 92121 Fax number: (619) 453-6991
APPLICANT: Phone number: (619) 453-0300
APPLICANT: Telex number:
TITLE OF INVENTION: Materials and Methods for the Control of
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Salivanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US94/07902
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Salivanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA79
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

PCT-US94-07902-30

Query 1734 AATAGATACTATAAGTGTGGAGCTCCCTAGTACCACTCCGCCAAC-----C 1783
Query 1802 CAATTATAATTATAATTCAATACTGGATTTCGAATTCCAAATTCGAAGTACAGT-- 1859
Query 1784 CAATGTCRACAGTTAACATTCAGATTCAGATTGGATGATGAAAGACAGTC 1843
Query 1860 -----ACATTACCTTAATTGAAACATACATTATAATTAACTGGAGATGTA 1912
Query 1844 CAATAAACATTTGAAGAGAACACTTAAIGCCCTTAAATGAAACATA 1903
Database 1845 CAATTCAATTAACTGGATGAAATTATCAAACTTAAATGAAACATA 1972
Database 1904 ATTCAATTATAATTATGGAAATTGAAATTCACATGATCTGATAG 1963
Query 1973 AAATAGAAGAAACAAATTAGAAACTTCAACAAAATAAACTTTTCACA 2032
Database 1964 ATTACAGAAGCAAAATTGAAATTAATGAAATAGATGATTGGTA 2023
Query 2033 ATCATACAAAAAAACTTAAATTAGA 2060
Database 2044 ATTAAACAAAGTCTTACTAAATTAGA 2051

Query 2 TGTTGTCAGGGAAATAACAAATAATGGTAGACATAATTGGTAGTGTGATACAA 61
Database 149 TGTGTCAGGATATCAGATATGGCATATAGCGGGAAATTGTTGTTGTAACAA 208
Query 62 TTCTGCGATTAGTCAGGTACTATGTTATCGGTACTCTGTTAGCCGGTATGGTGGGC 121
Database 209 TTCTTGAGTTACTGCACTGTTAGTGGAACTATGTTAGGAACTTGTGTCGCC 268
Database 122 TCACTCTTATATCGGACCGTAGGAAATAATTAATATCTTGTGACCC 181
Database 269 -----CTGCTTACCTGCAAGGTTATATCTTGTGACT 304
Query 182 TAATCACTGTCCTTGGCCCGCGGGAGAACAGAACATACTGGACACATTATA 241
Database 305 TGTGCGCATCTTGGCAGGATCTGCCCCG - - - - - CAAATGTTGGAGGTTGTTAA 361
Query 242 AAATGGGAAATTTTTGATACCCGTTACAGAAAGCATAAAAGCTAAAGTTAC 301
Database 362 ACATGGGAAAGCCATACAGAAATAAGATAAAAACATAATTATGTAACCTT-- 418
Database 419 ---CTATCCTAACACTCTAAAAATCACTGATAAAATCAGAAATTTCGATAAT 475
Query 302 AAACCTTAAAGGATTAGCAAAATAATPACAAAGCTTAAATCAGCATTAGATGTTGCA 361
Database 419 ---CTATCCTAACACTCTAAAAATCACTGATAAAATCAGAAATTTCGATAAT 475
Query 362 GAAATTAAAAAGACTAAAGCTCCTGGATTACCACTCATCGCATTACAAAGCTG 421
Database 476 GGGGCGCACGCTAACGCTAACGCTPAATGCTTAAGGAGTA-CATGATCTCTTACTACCTTA 534
Query 422 CCTTGACTCTTAAATTACGATTGAAATGTTGTCACAATGTTATTCGAAATACTG 481
Database 535 GAACTTAAATAGATAAAAGTTAGATGTTAAA-----571
Query 482 GTTTCGCAACTGAACTTAAACGCPATTACTACCTATTGCGCAGCTGCTTAATT 541
Database 572 --- - - - - - ATATGCTGACTCTGATAACACCTCCCTGATAACACACTCCCTGACAATAATGCTCT 625
Query 542 TTCAATTAAATTAAACAAAGGTGTGAATTTGCTGATGATGGAATGCGATATAAC 601
Database 626 GGCACTGTTGAAATTAAACATGCTGACCTPATACATGCTGCAAAATTCG 685
Query 602 ATCCCTCACAAATTGAACTTAATGCTGGAAACATGATGACTATTAAACTTTAAAG 661
Database 686 GT - - - - - ATAAATCAGACTCTCAATTACTATAGGGCTTAAAC 739
Query 662 AAAATATACCTTAATTATGAACTTATGCAATTACCTTATGAGGAGGACTAAATAAAC 721
Database 740 GTAATATACAGAAATTACTGACTATTGTTACAAACGTCACATATGTA 799
Query 722 TTGGAACGAACTTAAATGATGAGGATAATTAAATGTTATGAAAGATAATGACTA 781
Database 800 TTAGRACTAAACTAACGCAACATGGAATATGTTAGAATGACTC 859
Query 782 TTACTGTTAGATGACTATGCTCAATTCTTATGTTATGATAAAAGATAACAGATT 841
Database 860 TAATCTGTTAGATCTTATGCTTAAATTGACCCAGAAATA-----911
Query 842 CAATGGAAAGAATGGCATTAAACGAACTTACAGAAATTAAACGACTAGAA 901
Database 912 --- - - - - - TCCATTAGGTTAAATCTGAACTTACAGAACTTATGAGTTA 961
Query 902 TAAATTGACCTTAATCTGAACTTACCTGAAATTCAACCCAACTCCCTATAATGGAAATA 961
Database 962 --- - - - - - ATTCAAGATACTTGTGAACTTACAGAACTAGAA 997
Query 962 ATTAAACACGTTACGGCTTAAATGTTAGATTTCAATTGAACTTATGTTACAA 1021
Database 998 ATGGTTAACTAGAAATCTACATTACTGTTACAAACGGCGTTTACCAA 1057
Query 1022 AAAATGAAACGTTACGGAAATCGTTAGTTAGTGTGAAATCGTATAGATCTTATG 1081
Database 1058 GAAATTCCTCGAGACATTCTGATCCCTATGATATTGAAACCAGATGG 1117

GENERAL INFORMATION:

APPLICANT: Michaelis, Tracy Ellis
Foncerra, Luis

APPLICANT: Navva, Kenneth E.

TITLE OF INVENTION: Process for Controlling Scarab Pests
TITLE OF INVENTION: with Bacillus thuringiensis Isolates

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: David R. Salivanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0. Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/315,468

FILING DATE: 08/08/2003

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/014,941

FILING DATE: 01 FEB 1993

APPLICATION NUMBER: 07/828,430

FILING DATE: 30-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/808,316

FILING DATE: 16-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Salivanchik, David R.
REGISTRATION NUMBER: 31,794

REFERENCE/DOCKET NUMBER: MA73.C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 3507 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
STRAIN: kumamotoensis 5C
INDIVIDUAL ISOLATE: 5C

IMMEDIATE SOURCE:
LIBRARY: LambdaGEM-11 (tm) library of L. Foncerra
CLONE: 50C(b)

US-08-315-468-3

Query March 4, 4%; Score 92.6%; DB 2; Length 3507;
Best Local Similarity 44.7%; Pred. No. 3.5e-09;
Matches 683; Conservative 0; Mismatches 784; Indels 6;

Qy 429 TCTTAATAATAGATTTGAAAGATGTTCACATGTTTATTGCGAAATACTCGTTCCA 488

Db 504 TGTTCGAAATCGATTTGAAATCTCTGGATATGTTTACGGATAATAGCCATCTTGC 563

Qy 489 ACTTGAACATATAAACGTTTACTCATCTGTTGCAATTTTCAAA 548

Db 564 AGTGAAATAATTGAGNTTACATTCTTACAGTATACGGCGAACCTACATT 623

Qy 549 AAATTTTACACAGGTGCAATTGCTGAAATGCGATGATGGATCATACATCCTTC 608

Db 624 ACTTTTATTAGGGAGCATTAATTGAGATGG----- 663

Qy 609 ACAAAATGAAACTTAATGCTGAAACATCAGATGACTATTATAAACTTTAAAGAAATAT 668

RESULT 5
US-08-315-468-3
Sequence 3, Application US/08315468
Patent No. 5554534

Db	664	-----GGATTGTCCTAACAGCACTTAAACTATACTTAATGTCGAACCTAC 716	Db	1722 TCGGATTGGTTACGGCTCTAATGAACTAGTTATA-----TTAGTTT 1763	
Qy	669	ACCTAAATATAGTAACTATTGTGCAAATGAGGACTAATAAACTTGCATA 728	Qy	1749 ACCAGGAGTAATAGGAATACCACCTAACGACTCAACAGACACTTTCTGGTACAATTTA 1808	
Db	717	TGCGAATGATTCTGACCACTGTAAAGTGTTAGCAATTAAAAGG 776	Db	1764 ATACGGACTAACCAAGGGAACTTAAATTCAACAGACATATCTAAATAATGAA 1823	
Qy	729	CGAACCTAAATATGAGATGGAGTATTATGATTATGAAAGATATGACTTACGT 788	Qy	1809 TAATAATTACATAAGGAGATTTCGAGATTCCAACTCAGTAGTAACTTAC 1868	
Db	777	CTCGAGGGTAAACATGATTGACTAACCAATTCTCTAGAGAAATGACATTGAGGT 836	Db	1824 AAATGATTAAACATATAATGATTCAAAATAGAAATGAGTCATTGCTGAA 1883	
Qy	789	ATTAGATACTATCGCTCAATTTCCTTTATGATATAAAGGAGTACATTAGG 848	Qy	1869 TTAAATCGAAACATACATTATATTTAATGTTAATCGTGCAGTGTACAATTTTAA 1928	
Db	837	GTTGACCGTTGTGTCATTTCAAACTATGACTGCTTACCTP-----ATCCACTSGC 890	Db	1884 TGCTTCTCIAAACATACAGGGTTATCPATAGTATAACAAACGATAAAATTATTTAT 1943	
Qy	849	AAGATAGTGGGATTAANACTGAACTTAAAGGAAATTTATAACACTGAAATAATT 908	Qy	1929 CATTGATAAAATTGAAATTACATTACATT 1955	
Db	891	AAACACAGGTCAAGCTTACAGGGAGTATATCAGATCCACTGCGCT 950	Db	1944 TTAGACCGAATCGAATTCATCCAGT 1970	
Qy	909	TGACCGTCTTACCTACCTTACCTGAAATTCAACCCAATCTCGCTTAAATTTAAC 968	RESULT 6		
Db	951	TAATPATGGTCCTGGTAGACADAGCACCTCTCTCTAGAAATGAAAGGGCTRT 1010	US-08-349-867-22		
Qy	969	ACGTTCAGGGCTTAGATTATTTCATTTTAGATGAACTTATTTTACAAAAAAATCA 1028	Sequence 22, Application US/08349867		
Db	1011	TGCGTCACCTCATG---TGTGTTGATTATAACCGGACTCACACTTATAACAAAAACG 1067	; GENERAL INFORMATION:		
Qy	1029	AACCPACGGGAATCTTACTTGGTATGGAAATGCTACTATGCTACGCC 1088	; APPLICANT: Brad Fisch, Gregory A.		
Db	1068	TAGCTTCACT--TCTGATCGTTATGAGATATGGCTGGTCATCAATAAGTATAAG 1125	; APPLICANT: Thompson, Mark		
Qy	1089	AGGAACGTGAAATTATATGGAGAAAAGAACAGGGTCCACCCACAAACCTTAAATACC 1148	; APPLICANT: Schwab, George B.		
Db	1126	CATATGGTAGAGTAGTACACAGATGTTACAGATGTTACAGTAACTTCAGT 1185	; TITLE OF INVENTION: No. 5508264el Pesticidal Compositions		
Qy	1149	ATTGAACTCTTAAAGTTCACTTGAATGACTGTTACCTTACTCTTCCCCTT 1208	; NUMBER OF SEQUENCES: 34		
Db	1186	ACTCGCAATTGTTGATTTCAGAAATTAGCATTTACAGACTTTATCACATGGTCAGPA 1245	; CORRESPONDENCE ADDRESS:		
Qy	1209	TCCCTACATATACCTTACAAATTAAATGAACTTTAAATAATTCACCTAGTAA 1268	; ADDRESSEE: David R. Saliwanchik		
Db	1246	CTCCCTGATATAGTTACCTGTGTATACGTATACATTGTTGGATGCCGAAACCGAG 1305	; STREET: 2421 N.W. 41-st Street, Suite A-1		
Qy	1269	TAATAATTACATATTCTGGGGAAATTCTATGATAAAACACTGATTTCGA 1328	; CITY: Gainesville		
Db	1306	TTTTTTATGGTAAATGAAATGAAAGACCTTAACTTACCTATACCGCTTC 1365	; STATE: FL		
Qy	1329	ATTTCCTGTAATAAAAGACTGTAAACCAATTATTAATCACAATTTGCTTACCAAGSTATAA 1388	; COUNTRY: USA		
Db	1366	AA---AGATPATTATGATCGACAAATTAGGATCATAATTTACTTC 1421	; ZIP: 32606		
Qy	1389	TAGTTATGCTATTATTCAGTTTATTAAATTATCTTAAATTGTT 1448	; COMPUTER READABLE FORM:		
Db	1422	AGGTCAACCAATTAGGATCATAATGCAATTAGGATCATAATTACTTC 1481	; COMPUTER: IBM PC compatible		
Qy	1449	AGCGCTTAATATATTATAGGTTCAATTAGGTTGACAGACAGATTGCTTAAATGAA 1508	; OPERATING SYSTEM: PC DOS/MS-DOS		
Db	1482	CAGTTCACTAGCACCTGACCTGTTACCTGTTCTGACATCTGGAGTCAGATCTAAC 1541	; SOFTWARE: Patent In Release #1.0, Version #1.25		
Qy	1509	TAATGCAATTAGCATTAATTAATGATCCAGGAATCAAAAGGTAAACAGTCITGA 1568	; CURRENT APPLICATION DATA:		
Db	1542	AAATACAGTTAAAAGTCGGAATTCACCAAAATACCGGGCAACTCTACCACTAGG 1601	; APPLICATION NUMBER: US/08/349, 867		
Qy	1569	TACAAACTCAAGGTTAGGACCTGGTCAATAGGAGGAAACTTGGTTTATTACAA 1628	; FILING DATE: 09-07-2000		
Db	1602	CAGAAATCTTATATAAAAGGGCTGGTTACAGGGAGACTTGGCTTTAAC 1661	; ATTORNEY/AGENT INFORMATION:		
Qy	1629	AAGTCAGGGCTTTAGAGATTACATCTGAAACTCTTAATCTACAACTTTATTACAT 1688	; NAME: Saliwanchik, David R.		
Db	1662	GGACCGCATCGGAAGTGTGACTTCAAGTCTCAGGTCTCAACGTTTCGTT 1721	; REGISTRATION NUMBER: 31,794		
Qy	1689	TAGACTCTGATAGCTAACAAATGGTGTGAAATACTCTCTTACAAAT 1748	; REFERENCE/DOCKET NUMBER: MA86		
Db			; TELECOMMUNICATION INFORMATION:		
Qy			; TELEPHONE: 904-372-5800		
Db			; INFORMATION FOR SEQ ID NO: 22:		
Qy			; SEQUENCE CHARACTERISTICS:		
Db			; LENGTH: 3444 base pairs		
Qy			; TYPE: nucleic acid		
Db			; STRANDEDNESS: single		
Qy			; TOPOLOGY: linear		
Db			; MOLECULAR TYPE: DNA (genomic)		
Qy			; US-08-349-867-22		
Db			; Query Match 3 / 8; Score 79.6; DB 2;		
Qy			; Best Local Similarity 53.3%; Pred. No. 1.3e-06;		
Db			; Matches 212; Conservative 0; Mismatches 159; Indels 27; Gaps 1;		
Qy			; 436 ATACGATTGGAGAAATGTTCAACATTGTTTACCGAGAAATACCTGGTTCAACTTGC 495		
Db			; 388 ATTCCATTGCTAAACAGCAAGCGCTTTAACAGCAATAATTCTACATTACA 447		
Qy			; 496 ACTTAAATAAAGCTTATTACTACCTTAACTTGTAACTTCAATTAAATTTA 555		
Db			; 448 AGTTGAAATCCCTCTTATGGCTCATGGCAAGGGGAATTACATTACACTA 507		

Qy 556 TTACAAACAGGCTGTAATGGCTGATGAATGGAAATACTCCTCACAAATT 615
 Db 508 TTAGAGAGGCCTATCTTGGCAGCGCTGGACTCTGATAATTAAAT 567
 Qy 616 GRACCTAATGCTGGAACATCAGTGA CTTAAACTTAAAGAAAATAACCTAA 675
 Db 568 C----- ATTAAATAAGTAAATAATTCCATTAGA 600
 Qy 676 TATAGTAACATGTGCAAAATACCTTATGAGGACTAAAYAACCTGAGAACCT 735
 Db 601 TATACGAAACATGTTGGACACATACATCAGGATTGAAACCTAAGGTTCAATT 660
 Qy 736 AATATGAGTGGAGCTATTAACTTAACTGAGATATGACTTACGTATTAGAT 795
 Db 651 ACTGAGACATGGCAAGTCATAGTCATAGTCAGTTAGAGATTAACTACTGTTAGAT 720
 Qy 796 ACTATCGCTCAATTTCCTTTATGATAAAAGAGATA 833
 Db 721 ATCGTTGCCTTTCCGAACTAGCATGCTTAGAGATA 758

RESULT 7
 US-08-349-867-26
 Sequence 26, Application US/08349867
 Patent No. 550264
 GENERAL INFORMATION:
 APPLICANT: Bradisch, Gregory A.
 APPLICANT: Thompson, Mark
 APPLICANT: Schwab, George E.
 TITLE OF INVENTION: Improvement of Delta-Endotoxin Expression in
 NUMBER OF SEQUENCES: 34
 CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 ADDRESS: David R. Saliwanchik
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: FL
 COUNTRY: USA
 ZIP: 32606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/349,867
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Saliwanchik, David R.
 REGISTRATION NUMBER: MA86
 REFERENCE/DOCKET NUMBER: 31-794
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 904-375-8100
 TELEFAX: 904-372-5800
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3444 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)

US-08-349-867-26

Query Match Score 79.6; DB 2; Length 3444;
 Best Local Similarity 53.3%; Pred. No. 1.3e-06;
 Matches 212; Conservative 0; Mismatches 159; Indels 27; Gaps 1;

Qy 436 ATACGATTGAGAATGTTCACATGATTATTCTGAGAATACTGTTCAACTTGAA 495
 Db 388 ATCGATTGCTATACAGACGCTTAAATACGATAAAATTTACACTTACA 447
 Qy 496 ACTTATAAAACGCTTATTACTACCTATTATGCGCAAAGCTGCTAAATTAAATT 555

Db 448 AGTTTGAATCCCTTTATGGCTATGTCAGGGGAATTACATTACACTA 507
 Qy 556 TTACAAAGGGCTGATGAATGGAAATACTCCTCACAAATT 615
 Db 508 TTAGAGAGGCCTATCTTGGCAGCGCTGGACTCTGATAATTAAAT 567
 Qy 616 GRACCTAATGCTGGAACATCAGTGA CTTAAACTTAAAGAAAATAACCTAA 675
 Db 568 C----- ATTAAATAAGTAAATAATTCCATTAGA 600
 Qy 676 TATAGTAACATGTGCAAAATACCTTATGAGGACTAAAYAACCTGAGAACCT 735
 Db 601 TATACGAAACATGTTGGACACATACATCAGGATTGAAACCTAAGGTTCAATT 660
 Qy 736 AATATGAGTGGAGCTATTAACTTAACTGAGATATGACTTACGTATTAGAT 795
 Db 661 ACTGAGACATGGCAAGTCATAGTCATAGTCAGTTAGAGATTAACTACTGTTAGAT 720
 Qy 796 ACTATCGCTCAATTTCCTTTATGATAAAAGAGATA 833
 Db 721 ATCGTTGCCTTTCCGAACTAGCATGCTTAGAGATA 758

RESULT 8
 US-08-239-476-22
 Sequence 22, Application US/08239476
 Patent No. 5527893
 GENERAL INFORMATION:
 APPLICANT: Thompson, Mark
 APPLICANT: Schwab, George E.
 TITLE OF INVENTION: Improvement of Delta-Endotoxin Expression in
 NUMBER OF SEQUENCES: 34
 CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David R. Saliwanchik
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: Florida
 COUNTRY: USA
 ZIP: 32606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0 Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/239,476
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Saliwanchik, David R.
 REGISTRATION NUMBER: 31-794
 REFERENCE/DOCKET NUMBER: MA83
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (904) 375-8100
 TELEFAX: (904) 372-5800
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3444 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)

US-08-239-476-22

Query Match Score 79.6; DB 2; Length 3444;
 Best Local Similarity 53.3%; Pred. No. 1.3e-06;
 Matches 212; Conservative 0; Mismatches 159; Indels 27; Gaps 1;

Qy 436 ATACGATTGAGAATGTTCACATGATTATTCTGAGAATACTGTTCAACTTGAA 495
 Db 388 ATCGATTGCTATACAGACGCTTAAATACGATAAAATTTACACTTACA 447
 Qy 496 ACTTATAAAACGCTTATTACTACCTATTATGCGCAAAGCTGCTAAATTAAATT 555

Query Match Similarity 3.8%; Score 79.6; DB 2; Length 3444;
 Best Local Similarity 53.3%; Pred. No. 1.3e-06; Indels 27; Gaps 1;
 Matches 212; Conservative 0; Mismatches 159; Indels 27; Gaps 1;
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 US-08-598-305A-26

Query Match Similarity 3.8%; Score 79.6; DB 2; Length 3444;
 Best Local Similarity 53.3%; Pred. No. 1.3e-06; Indels 27; Gaps 1;
 Matches 212; Conservative 0; Mismatches 159; Indels 27; Gaps 1;
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 US-08-598-305A-26

Qy 436 ATACGATTGAGAATGTCACATGATTATTATTCGAGAAATACTCGTTCAACTTGAA 495
 Db 388 ATTGCAATTGCTTAAACAGCAGCTTAAATTAATTTACACITACA 447
 Qy 496 ACTTATAAACCTTAATFACTACCTTAATTTATGGCAAGCTGTAAATTAAATTAA 555
 Db 448 AGTTTGAATCCCTCTTATCGGCTCTATGTTCAAGCGGAATTACATTATGACTA 507
 Qy 556 TTACAACAGGTGCTGAAATGGCTGTGATGAAATCGAGATACTCGTCAAATT 615
 Db 508 TTAAGAACGCTGTATGGTGGAGCTGGAGATGGTAAATTAAATTAATTAATTAAT 567
 Qy 616 GAACCTTAATGCTGGAACATCAGATGACTATTAAACTTTAAAAGAAATACTCAA 675
 Db 568 C-----ATTATAATAGATAATTAAATCTTATTCTATAGA 600
 Qy 676 TATAGTACTATGCTGAAATACCTATAGAGAGGACTAAATTAACCTCGAACGCC 735
 Db 601 TATAGAACATGTTGGACACATACAACTCAGGATTGAAACCTTAAAGGGTAAAT 660
 Qy 736 AATATGAGATGGAGATATTAAATGATTATGGAGATAATGACTATTCTGTTAGAT 795
 Db 661 ACTCGACATGGCAAGATCATCAGTTAGAGATTTACACTTACCTGTATAGAT 720
 Qy 796 ACTATCGCTCAATTCTTATGATATAAGAGATA 833
 Db 721 ATCGTTGCTCTTTCGAACTACGATGTAAACATA 758

RESULT 11
 US-08-598-305A-26
 ; Sequence 26, Application US/08598305A
 ; Patent No. 5827514
 ; GENERAL INFORMATION:
 ; APPLICANT: BRADFISCH, Gregory A.
 ; APPLICANT: THOMPSON, Mark A.
 ; APPLICANT: SCHWAB, George E.
 ; TITLE OF INVENTION: No. 5827514el Pesticidal Compositions
 ; NUMBER OF SEQUENCES: 38
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Salivanchik, Lloyd & Salivanchik
 ; STREET: 2421 N.W. 41st Street, Suite A-1
 ; CITY: Gainesville
 ; STATE: FL
 ; COUNTRY: USA
 ; ZIP: 32606-6669
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/598, 305A
 ; FILING DATE: 08-FEB-1996
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sanders, JAY M.
 ; REGISTRATION NUMBER: 39, 355
 ; REFERENCE DOCKET NUMBER: MA86.D1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 352-375-8100
 ; TELEFAX: 352-372-5800
 ; INFORMATION FOR SEQ ID NO: 26:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3444 base pairs

RESULT 12
 US-08-639-923A-22
 ; Sequence 22, Application US/08639923A
 ; Patent No. 5840554
 ; GENERAL INFORMATION:
 ; APPLICANT: Thompson, Mark K.
 ; APPLICANT: Schwab, George E.
 ; TITLE OF INVENTION: Improvement of Delta-Endotoxin Expression in
 ; Pseudomonas fluorescens
 ; NUMBER OF SEQUENCES: 38
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: David R. Salivanchik
 ; STREET: 2421 N.W. 41st Street, Suite A-1
 ; CITY: Gainesville
 ; STATE: Florida
 ; COUNTRY: USA
 ; ZIP: 32606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/639, 923A
 ; FILING DATE: 24-APR-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/639, 923A
 ; FILING DATE: 06-MAY-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Salivanchik, David R.
 ; REGISTRATION NUMBER: 31, 794
 ; REFERENCE/DOCKET NUMBER: MA83.D1

Page 11

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/05431
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Saliwanchik, David R.
 REGISTRATION NUMBER: 31,794
 REFERENCE/DOCKET NUMBER: MA83
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (904) 375-8100
 TELEFAX: (904) 372-5800
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3444 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 PCT-US95-05431-22

Query Match 3.8%; Score 79.6; DB 6; Length 3444;
 Best Local Similarity 53.3%; Pred. No. 1.3e-16;
 Matches 212; Conservative 159; Indels 27; Gaps 1;

Qy 436 ATACGATTGAGATGTACATGATTATTCGAGAAATACCTGTCCACTGTAA 495
 Db 388 ATTCGATTGCTTATAACGACGCGCTTTAACACGCAATAAATTTAACATCA 447

Qy 496 ACTTAAACGGCTTAACTACCTATTATGCCAAGCTGTAATTTCATTAAATTAA 555
 Db 448 AGTTTGAAATCCCTCTTTATCGGTCTATGTCAACGGCATTACATTATCACA 507

Qy 556 TTACAAACGGCTGTGAATTGGCTGATGAAATGCAATCTCICAACATT 615
 Db 508 TTAAGAGACGCTTATCCTTGGCAGGGTGGGACTATGGATATGCTGTAAAT 567

Qy 616 GAACCTAATGCTGGAAACATCAGTGAATGCAATGAGATAACATCTCICAACATT 675
 Db 568 C-----ATTATATGATTAATAATCTTATTCTATAGA 600

Qy 676 TATAGTAACATTGGCAAATACCTATAGAGAGGACTAAACTTCGAAGACACT 735
 Db 601 TATACGAAACATGTTGGACACATACAGGATTAAGAACCTAAAGGTTAAAT 660

Qy 736 AATATGAGATGGAGTATTATGATGAAATATGCACTTACATGTTATTAGAT 795
 Db 661 ACTCGACAAATGGCCAAGATCATCAGTTAACCTTAAGGAGTTAACATCA 720

Qy 796 ACTATGCTCAATTCTTTATGATATAAGAGATA 833
 Db 721 ATCGTTGCTCTTTTCGAACTACGAGTTAACATCA 758

RESULT 15
 PCT-US95-05431-26
 Sequence 26, Application PC/TUS9505431
 GENERAL INFORMATION:
 APPLICANT: Street address: 5501 Oberlin Drive
 APPLICANT: City: San Diego
 APPLICANT: State/Province: California
 APPLICANT: Country: US
 APPLICANT: Postal code/Zip: 92121
 APPLICANT: Phone number: (619) 453-8030
 APPLICANT: Telex number: 601 453-8030
 TITLE OF INVENTION: Improvement of Delta-Endotoxin Expression in
 TITLE OF INVENTION: Pseudomonas fluorescens
 NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:
 ADDRESSEE: David R. Saliwanchik
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: Florida
 COUNTRY: USA
 ZIP: 32606

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-POS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/05431
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Saliwanchik, David R.
 REGISTRATION NUMBER: 31,794
 REFERENCE/DOCKET NUMBER: MA83
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (904) 375-8100
 TELEFAX: (904) 372-5800
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3444 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 PCT-US95-05431-26

Query Match 3.9%; Score 79.6; DB 6; Length 3444;
 Best Local Similarity 53.3%; Pred. No. 1.3e-16;
 Matches 212; Conservative 0; Mismatches 159; Indels 27; Gaps 1;

Qy 436 ATACGATTGAGAAATGTTCAAAATGTTTATTCGAGAAATACCTGTCCACTGTAA 495
 Db 388 ATTCGATTGCTTATAACGACGCGCTTTAACACGCAATAAATTTAACATCA 447

Qy 496 ATCTTAAACGGCTTAACTACCTATTATGCCAAGCTGTAATTTCATTAAATTAA 555
 Db 448 ATTCGATTGCTTATAACGACGCGCTTTAACACGCAATAAATTTAACATCA 447

Qy 556 TTACAAACGGCTGTGAATTGGCTGATGAAATGCAATCTCICAACATT 615
 Db 508 TTAAGAGACGCTTATCCTTGGCAGGGTGGGACTATGGATATGCTGTAAAT 567

Qy 616 GAACCTAATGCTGGAAACATCAGTGAATGCAATGAGATAACATCTCICAACATT 675
 Db 568 C-----ATTATATGATTAATAATCTTATTCTATAGA 600

Qy 676 TATAGTAACATTGGCAAATACCTATAGAGAGGACTAAACTTCGAAGACACT 735
 Db 601 TATACGAAACATGTTGGACACATACAGGATTAAGAACCTAAAGGTTAAAT 660

Qy 736 AATATGAGATGGAGTATTATGATGAAATATGCACTTACATGTTATTAGAT 795
 Db 721 ATCGTTGCTCTTTTCGAACTACGAGTTAACATCA 758

Qy 796 ACTATGCTCAATTCTTTATGATATAAGAGATA 833
 Db 721 ATCGTTGCTCTTTTCGAACTACGAGTTAACATCA 758

Qy 796 ACTATGCTCAATTCTTTATGATATAAGAGATA 833
 Db 721 ATCGTTGCTCTTTTCGAACTACGAGTTAACATCA 758

Search completed: February 15, 2006, 03:31:12
 Job time : 384 secs

Result No.	Score	Query Match	Length	DB ID	Description
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2	2085	100.0	2235	8	US-10-782-570-1
3	1794.4	86.1	2208	8	US-10-783-417-1
4	161.2	7.7	4896	3	US-09-756-526A-3
5	161.2	7.7	4896	6	US-10-345-120-3
6	161.2	7.7	4896	6	US-10-342-821-3
c 7	117	5.6	1548	6	US-10-311-455-2128
c 8	100.6	4.8	3684	9	US-10-929-54-2
c 9	99.2	4.8	3673778	6	US-10-312-841-1
c 10	93.6	4.5	8056	8	US-10-473-126-386
c 11	86.8	4.2	8056	8	US-10-473-126-240
c 12	83.2	4.0	8056	8	US-10-473-126-386
c 13	79.6	3.8	3522	3	US-09-826-660-5
c 14	79.6	3.8	3522	3	US-09-837-961-7
c 15	79.6	3.8	3522	8	US-10-825-751-7
c 16	77.8	3.7	3504	5	US-10-089-678-3
c 17	77.8	3.7	3690	5	US-10-089-678-3
c 18	77.2	3.7	1959	7	US-10-614-076-13
c 19	77	3.7	18154	6	US-10-311-455-227
c 20	76.4	3.7	8056	8	US-10-73-126-240
c 21	75.6	3.6	1482	7	US-10-614-076-69
c 22	75.6	3.6	1956	7	US-10-614-076-51
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c 24	75.6	3.6	1959	5	US-10-614-076-51
c 25	75.6	3.6	1959	7	US-10-614-076-1
c 26	75.6	3.6	1959	7	US-10-614-076-15
c 27	75.6	3.6	1959	7	US-10-614-076-17
c 28	75.6	3.6	1959	7	US-10-614-076-19
c 29	75.6	3.6	1959	7	US-10-614-076-23
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c 31	75.6	3.6	1959	7	US-10-614-076-27
c 32	75.6	3.6	1959	7	US-10-614-076-31
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c 35	75.6	3.6	1959	7	US-10-614-076-37
c 36	75.6	3.6	1959	7	US-10-614-076-43
c 37	75.6	3.6	1959	7	US-10-614-076-45
c 38	75.6	3.6	1959	7	US-10-614-076-59
c 39	75.6	3.6	1959	7	US-10-614-076-65
c 40	75.6	3.6	1959	7	US-10-614-076-67
c 41	75.6	3.6	1959	7	US-10-614-076-97
c 42	75.6	3.6	1959	7	US-10-614-076-99
c 43	75.6	3.6	2280	7	US-10-614-076-102
c 44	75.6	3.6	5930	6	US-10-311-455-490
c 45	75	3.6	5930	6	US-10-311-455-490

Db	181	CATATCACTGCTTTGGCCGGGAAACAGAACAAACAGTGGACACATTATT	240	Qy	1321	GATTTCAATTCCGTAAAGCTGTAACCAATTAAATGTTACCA	1380
Qy	241	AAATGGGAAATTTTGTGATAACCGTTAACGAAAGCATAAAAGCTAAAGTTA	300	Db	1321	GATTTCAATTCCGTAAAGCTGTAACCAATTAAATGTTACCA	1380
Qy	241	AAATGGGAAATTTTGTGATAACCGTTAACGAAAGCATAAAAGCTAAAGTTA	300	Db	1381	AGCTATAATAGTTATAGTCATATTTCATCCCAGTTCTTATTCCATATAAA	1440
Qy	301	CAACTTAGAGGATTAGACAATTATAAACGTTATAACGCTTACAGTGTGATG	360	Db	1381	AGCTATAATAGTTATAGTCATATTTCATCCCAGTTCTTATTCCATATAAA	1440
Qy	301	CAAACTTAGAGGATTAGACAATTATAAACGCTTACCGTTAACGAAAGCATAAAAGCTAAAGTTA	360	Db	1441	ATGGATTAGCGTAATAATTATACAGTGTGCAATTAGATGGACACAGTGCTT	1500
Qy	361	AGAAAATTAAAGACTACAAGCTCTGGATTACCCATCATCGATTACACAGT	420	Db	1441	ATGGATTAGCGTAATAATTATACAGTGTGCAATTAGATGGACACAGTGCTT	1500
Qy	361	AGAAAATTAAAGACTACAAGCTCTGGATTACCCATCATCGATTACACAGT	420	Db	1441	ATGGATTAGCGTAATAATTATACAGTGTGCAATTAGATGGACACAGTGCTT	1500
Db	421	GCCTTGACTCTTAAATACGTTGAGATGTTCAACATGATTATTGAGAAATACTT	480	Qy	1501	AATAGAAATAATGCAATTAGATAATTACATGATGTTACAGTGCTT	1560
Db	421	GCCTTGACTCTTAAATACGTTGAGATGTTCAACATGATTATTGAGAAATACTT	480	Db	1501	AATAGAAATAATGCAATTAGATAATTACATGATGTTACAGTGCTT	1560
Qy	481	GTTTCCAACTGAACTTAAACGTTTACTCTTATGCCAAGCTGCTTAT	540	Qy	1561	AGTCITGATAACAACTCTAACGACCTGTTCAACAGAGAACACTGTT	1620
Qy	481	GTTTCCAACTGAACTTAAACGTTTACTCTTATGCCAAGCTGCTTAT	540	Db	1561	AGTCITGATAACAACTCTAACGAGCGTTAGATGGACCTGTT	1620
Qy	541	TTCATTAATTACACAGGTTGATGAAATGGATGAGATA	600	Db	1621	TATTCAAAAGTCAGGGCTTTAGAGATACTGAGAAACTCTTCAACATCT	1680
Qy	541	TTCATTAATTACACAGGTTGATGAAATGGATGAGATA	600	Db	1621	TATTCAAAAGTCAGGGCTTTAGAGATACTGAGAAACTCTTCAACATCT	1680
Db	601	CATCCCTCACAAATTGAACTTAACGCTTAATGCTGAACTCATTAAACTTTAAA	660	Qy	1681	TATTACATTAGACTCTAGCTTACAAATTGCTGAAATACTCTTCAATATCT	1740
Qy	601	CATCCCTCACAAATTGAACTTAACGCTTAATGCTGAACTCATTAAACTTTAAA	660	Db	1681	TATTACATTAGACTCTAGCTTACAAATTGCTGCTGAAATACTCTTCAATATCT	1740
Db	661	GAAAATACCTAAATATGAACTATGCTATGAGGACTAAATA	720	Qy	1741	CTTACAAATTACAGGAGTAATTAGGAAATACCACCTCAACGACTCAACACTTCTGTT	1800
Qy	661	GAAAATACCTAAATATGAACTATGCTATGAGGACTAAATA	720	Db	1741	CTTACAAATTACAGGAGTAATTAGGAAATACCACCTCAACGACTCAACACTTCTGTT	1800
Db	721	CITCGAAACGAACTCTAAATGAGATGGATGAACTTATGACT	780	Qy	1801	ACAAATTATAATTACATACGGAGATTTCGTTTCAATTCCAAAGTACAGTA	1860
Qy	721	CITCGAAACGAACTCTAAATGAGATGGATGAACTTATGACT	780	Db	1801	ACAAATTATAATTACATACGGAGATTTCGTTTCAATTCCAAAGTACAGTA	1860
Db	781	ATTACTGTTAGATCACTATGCTCATTTCATGGATGATGTTATGACT	840	Qy	1861	ACATTACCTTTAAATGAAACATACATTATATTAAATCTGCAATTAATTCA	1920
Qy	781	ATTACTGTTAGATCACTATGCTCATTTCATGGATGATGTTATGACT	840	Db	1861	ACATTACCTTTAAATGAAACATACATTATATTAAATCTGCAATTAATTCA	1920
Db	841	TCAATGGAAAGTATGGGCAATTAACTGAACCTTAAATGAACTTAA	900	Qy	1921	ATTTTAAATCTTGTATAAAATTGAAATTATACCAATTACTTCCTGCAAGTAAATAGA	1980
Qy	841	TCAATGGAAAGTATGGGCAATTAACTGAACCTTAAATGAACTTAA	900	Db	1921	ATTTTAAATCTTGTATAAAATTGAAATTATACCAATTACTTCCTGCAAGTAAATAGA	1980
Db	901	ATAAAATTGACCGCTTACTTACCTGAAATTCAACCCAACTCGCTTAAATGAA	960	Qy	1981	GAAGAACAAATTAGAAACTATCCAAACAAATTAAATCATTTTCAACATCATACA	2040
Qy	901	ATAAAATTGACCGCTTACTTACCTGAAATTCAACCCAACTCGCTTAAATGAA	960	Db	1981	GAAGAACAAATTAGAAACTATCCAAACAAATTAAATCATTTTCAACATCATACA	2040
Db	961	ATAATACGCTTCAGGCTTACATTCTTACATGAAATTCAACCCAACTCGCTTAAATGAA	1020	Qy	2041	AAAAATACCTTTAAATAGAGCCACAACTATGATAATTGTTAA	2085
Qy	961	ATAATACGCTTCAGGCTTACATTCTTACATGAAATTCAACCCAACTCGCTTAAATGAA	1020	Db	2041	AAAAATACCTTTAAATAGAGCCACAACTATGATAATTGTTAA	2085
Db	1021	AAAATGAAACCTACGGAAATTCAACCCAACTCGCTTAAATGAA	1080	Qy	RESULT 2		
Db	1021	AAAATGAAACCTACGGAAATTCAACCCAACTCGCTTAAATGAA	1080	Db	US-10-782-570-1		
Qy	1081	GCTAGGACAGAACTGAAATTATAATGGAAGAAACAGGTGTCACCCACAAACAAACT	1140	Qy	Sequence 1, Application US/10782570		
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Qy	1141	TAAATACCATGAACTCTTAAAGTTCAATGCTAATGAACTTAACTCCCTACT	1200	Db	; APPLICANT: Carozzi, Nadine		
Qy	1201	TCCCCCTTTCTAACATACATTCAATTGAAATTGAACTTAAATATCA	1260	Qy	; APPLICANT: Hargiss, Tracy		
Qy	1201	TCCCCCTTTCTAACATACATTCAATTGAAATTGAACTTAAATATCA	1260	Db	; APPLICANT: Koziel, Michael G.		
Qy	1261	CTCTGAAATTAAATTAACATTCAGCTGGGGAAATTATCTATGATAATTGAA	1320	Qy	; APPLICANT: Duct, Nicholas B.		
Qy	1261	CTCTGAAATTAAATTAACATTCAGCTGGGGAAATTATCTATGATAATTGAA	1320	Db	; APPLICANT: Carr, Brian		
); TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and			
				; FILE REFERENCE: 045610/274144			
				; CURRENT APPLICATION NUMBER: US/10782570			
				; PRIORITY FILING DATE: 2004-02-19			
				; NUMBER OF SEQ ID NOS.: 17			
				SOFTWARE: FastSDS for Windows Version 4.0			

;	SEQ ID NO 1	901	ATTAATTTTGACCGTCTTACTTACCTGAAATTCAACCCAATCTCCGTATAATGGAAAT	960
;	LENGTH: 2235	1051	ATTAATTTGACCGTCTTACTTACCTGAAATTCAACCCAATCTCCGTATAATGGAAAT	1110
;	ORGANISM: Bacillus thuringiensis	961	ATTAATACACGGTCAGGCTTAGATATTTCATTAGTGAACCTATATTATTAATACA	1020
;	FEATURE: CDS	1111	ATTAATACACGGTCAGGCTTAGATATTTCATTAGTGAACCTATATTATTAATACA	1170
;	NAME/KEY: LOCATION: (1) ... (2235)	1021	AAAATGAAACCTACGGGAATCGTGTAGTTAGTGAATGCTACTAT	1080
;	us-10-782-570-1	1171	AAAATGAAACCTACGGGAATCGTGTAGTTAGTGAATGCTACTAT	1230
Qy	Query Match, Similarity 100.0%, Score 2085, DB 8, Length 2235;	1081	GCTACAGACAGGAACTGAAATTATATGGAAGAACAGGTCACCCACAAACT	1140
Db	Best Local Similarity 100.0%, Pred. No. 0, Mismatches 0; Indels 0; Gaps 0;	1231	GCTACAGACAGGAACTGAAATTATATGGAAGAACAGGTCACCCACAAACT	1290
Qy	1 ATGNGTCAAAGGAAATAACAAATATGGTATAATTTCGAGACATTGCTAGTGTATA	60	1201 TCCCTCTTCCTAACATACTTACATTAACTCAATTAACTAATTAATTAATCA	1260
Db	151 ATGNGTCAAAGGAAATAACAAATATGGTATAATTTCGAGACATTGCTAGTGTATA	210	1291 TAAATACCTTCTAACATACTTACATTAACTCAATTAACTAATTAATTAATCA	1350
Qy	61 ATGCTGCGTTAGTCGAGTGTACTATGTTAGCGGTACTCTGTAGGTCG	120	1351 TCCCTCTTCCTAACATACTTACATTAACTCAATTAACTAATTAATTAATCA	1410
Db	211 ATGCTGCGTTAGTCGAGTGTACTCTGTAGGTCG	270	1361 CCTAGTAATAATTAACTACATTCAGCTGGGGAAATTATCTAACTTAACTTAA	1320
Qy	121 CTCACTTCATATCGGACCGATAGGATAATAGTGTCTATAATATGGTAC	180	1411 CCTAGTAATAATTAACTACATTCAGCTGGGGAAATTATCTAACTTAACTTAA	1470
Db	271 CTCACTTCATATCGGACCGATAGGATAATAGTGTCTATAATATGGTAC	330	1321 GATTTCATTTCCTGAAACCAATTAACTTCAGCTTAACTTAACTTAACTTAA	1380
Qy	181 CTAACTCACTGCTTTGGCCCGGGAGAACAGAACAAACACTATGCCAACAACTT	240	1471 GATTTCATTTCCTGAAACCAATTAACTTCAGCTTAACTTAACTTAACTTAA	1530
Db	331 CTAATCACTGCTTTGGCCCGGGAGAACAGAACAACTTAACTTAACTTAA	390	1381 AGCTTAATAGTGTATAGTCATTTATCAGCTTAACTTAACTTAACTTAACTTAA	1440
Qy	241 AAAATGGGAAATTGGTGTATAACCGTTAACAGAACATAAAACGTPAAAGTA	300	1531 AGCTTAATAGTGTATAGTCATTTATCAGCTTAACTTAACTTAACTTAACTTAA	1590
Db	391 AAAATGGGAAATTGGTGTATAACCGTTAACAGAACATAAAACGTPAAAGTA	450	1441 ATTCGATTAGCGCTAAATTATATTATACAGCTGCTATTAGGATGACACAGTAGTGT	1500
Qy	301 CAAACTTGAAGGATTAGCAAATAATTACAAAGCTATAACGATAGTGTG	360	1591 ATTCGATTAGCGCTAAATTATATTATACAGCTGCTATTAGGATGACACAGTAGTGT	1650
Db	451 CAAACTTGAAGGATTAGCAAATAATTACAGTGTGAACTATAACGATAGTGTG	510	1501 AATAGAAATAATGAAATTCAGATAATGCTCCAGCAATCAAGGTAA	1560
Qy	361 AGAAATTAAAGACTAAAGCCTGCCTGGATTACCCATCATCACAAAGCT	420	1651 AATAGAAATAATGAAATTCAGATAATGCTCCAGCAATCAAGGTAA	1710
Db	511 AGAAAATTAAAAGACTACAGCTCCTGGATTACCCATCATCACAAAGCT	570	1561 AGCTCTGATAACAACTCTAAGGTAAATGAGGACCTGGTCATACAGGAAACTGTGT	1620
Qy	422 GCCTTGACTCTTAAATACCTTGAATGTTCAATGATTTCATTGGAATAACT	480	1711 AGTCGTGATAACAACTCTAAGGTAAATGAGGACCTGGTCATACAGGAAACTGTGT	1770
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Qy	481 GGTTTCCAACTTGAACCTATAAAACGTTAACCTACGTTATGCGAGGTGTAACT	540	1771 TATTACAAAGTCAGGGCGTTAGAGGATTACATGTTAGAACTCTTAACTCACAACT	1830
Db	631 GGTTTCCAACTTGAACCTATAAAACGTTAACCTACGTTATGCGAGGTGTAACT	690	1681 TATTACATTTAGGTTAGGAAATTCAGGAAATTCAGGAAATTCAGGAAATTCAGGAA	1740
Qy	541 TTTCATTAAATTAACTTACAAACAGGTGTGAAATTGGCTGAAATTGGCTGAA	600	1831 TATTACATTTAGGTTAGGAAATTCAGGAAATTCAGGAAATTCAGGAAATTCAGGAA	1890
Db	691 TTTCATTAAATTAACTTACAAACAGGTGTGAAATTGGCTGAAATTGGCTGAA	750	1741 CTTACAAATTACCGGGATAATTAGGAAATTCAGGAAATTCAGGAAATTCAGGAA	1800
Qy	601 CATCCPTCAAACTTGAACCTAATGCTGGACATCATGAACTTAACTTAA	660	1891 CTTACAAATTACCGGGATAATTAGGAAATTCAGGAAATTCAGGAAATTCAGGAA	1950
Db	751 CATCCPTCAAACTTGAACCTAATGCTGGACATCATGAACTTAACTTAA	810	1801 ACAAAATTATAATTAACTTACATAACGGGATAATTCCAGTAACTTTCAGTAACT	1860
Qy	661 GAAAATATCCTAAATTATGAACTATTGTCGAAATTAACTTAACTTAA	720	1951 ACAAAATTATAATTAACTTACATAACGGGATAATTCCAGTAACTTTCAGTAACT	2010
Db	811 GAAAATATCCTAAATTATGAACTATTGTCGAAATTAACTTAACTTAA	870	1861 ACATACCTTTAACTGAAACATACATTATACTTAACTGCTGAAATTCAATTCA	1920
Qy	721 CTTCGAAACGAAACCTTAATATGAACTTAACTGAACTTAACTTAACTTAA	780	2011 ACATACCTTTAACTGAAACATACATTATACTTAACTGCTGAAATTCAATTCA	2070
Db	871 CTTCGAAACGAAACCTTAATATGAACTTAACTGAACTTAACTTAACTTAA	930	1921 ATTAAATCATTGATAAAATTGAAATTTCAGGAAATTCAGGAAATTCAGGAAATTCAG	1980
Qy	781 ATTACTGTTAGAATGCTCAATTCTCTTTATGATAAGAGATAACAGAT	840	2071 ATTAAATCATTGATAAAATTGAAATTTCAGGAAATTCAGGAAATTCAGGAAATTCAG	2130
Db	931 ATTACTGTTAGAATGCTCAATTCTCTTTATGATAAGAGATAACAGAT	990	1981 GAAAACAAAAATTAGAAACTATCCAAACAAAAATTACATTTCAAAATCATACA	2040
Qy	841 TCAATAGGAAAGATACTGGCATTAAAACTGAACTTACAAAGAAATTATACTGAA	900		
Db	991 TCAATAGGAAAGATACTGGCATTAAAACTGAACTTACAAAGAAATTATACTGAA	1050		
Qy				

Db	2131	GAAAAACAAAATTAGAAACTATCCAAAACAAACTATGATACTTCAAAAATCATACA	2190	
Qy	2041	AAAATACCTTAATATAGAAAGCRAAACATGATGATGTTCAAAAATCATATAA	2055	
Db	2191	AAAATACCTTAATATAGAAAGCRAAACATGATGATGTTCAAAAATCATATAA	2235	
RESULT 3 US-10-783-417-1				
Sequence 1: Application US/10783417				
Publication No. US200402161861				
GENERAL INFORMATION:				
APPLICANT: Carozzi, Nadine				
APPLICANT: Hargiss, Tracy				
APPLICANT: Koziel, Michael G.				
APPLICANT: Duck, Nicholas B.				
APPLICANT: Carr, Brian				
TITLE OF INVENTION: AXM1-006, A Delta-Endotoxin Gene and				
TITLE OF INVENTION: Methods for Its Use				
FILE REFERENCE: 04560/274146				
CURRENT APPLICATION NUMBER: US/10/783,417				
CURRENT FILING DATE: 2004-02-20				
PRIOR APPLICATION NUMBER: 60/448,806				
PRIOR FILING DATE: 2003-02-20				
NUMBER OF SEQ ID NOS: 15				
SOFTWARE: fastSEQ for Windows Version 4.0				
SEQ ID NO 1				
LENGTH: 2208				
TYPE: DNA				
ORGANISM: <i>Bacillus thuringiensis</i>				
FEATURE: CDS				
NAME/KEY: CDS				
LOCATION: (1) ... (2208)				
US-10-783-417-1				
Query Match Score 1794.4; DB 8; Length 2208; Best Local Similarity 92.7%; Pred. No. 0; Matches 1908; Conservative 0; Mismatches 141; Indels 9; Gaps 2;				
Qy	1	ATGGTCAGG3AATACACAATATGGTATAATTGAGACAACTTGTAGTGTGATACA	60	
Db	154	ATGGTCAGG3AATACACAATATGGTATAATTGAGACAACTTGTAGTGTGATACA	213	
Qy	61	ATGGTCAGG3AATACACAATATGGTATAATTGAGACAACTTGTAGTGTGATACA	120	
Db	214	ATGGTCAGG3AATACACAATATGGTATAATTGAGACAACTTGTAGTGTGATACA	273	
Qy	121	CTGACTCTTATATCGGAAGCAGTAGGAAATATGGTATAATTGAGACAACTTGTAGTGTGATACA	180	
Db	274	CTGACTCTTATATCGGAAGCAGTAGGAAATATGGTATAATTGAGACAACTTGTAGTGTGATACA	333	
Qy	181	CTAACATCACTGTCCTTTGCCCGGGAGAACAGACAAAAACTATGGACAACTTGTAGTGTGATACA	240	
Db	334	CTAACATCACTGTCCTTTGCCCGGGAGAACAGACAAAAACTATGGACAACTTGTAGTGTGATACA	393	
Qy	241	AAATGGCAGAAATTGGTGTAGACCGTTAACAGAAAGCTAAACAGCTAAAGTA	300	
Db	394	AAATGGCAGAAATTGGTGTAGACCGTTAACAGAAAGCTAAACAGCTAAAGTA	453	
Qy	301	CAACATTGAAAGGATTAGACAATATAAGCTTACGATTAGTAGTGTGATGATG	360	
Db	454	CAACATTGAAAGGATTAGACAATATAAGCTTACGATTAGTAGTGTGATGATG	513	
Qy	361	AGAAAATTAAAGGACTACAAGCTTACGATTACGATGAACTTACGATTACACAAGT	420	
Db	514	AGAAAATTAAAGGACTACAAGCTTACGATTACGATGAACTTACGATTACACAAGT	573	
Qy	421	GCCTTGACTCTTAAATCGATTGAGATGTTCAATGTTATTCGAGAAATACCT	480	
Db	574	GCCTTGACTCTTAAATCGATTGAGATGTTCAATGTTATTCGAGAAATACCT	633	
Qy	481	GGTTTCCAACCTGAAACCTTACCTTAAACGTTATGAGGACCTGTTACACGAAAC	540	

Db 1711 GGTAAACAATCTTGATAACAAACTCTAAGGTAATTGGAGGCCATACAGGGAAAC 1770 ; DATE: 1999-06-18
 ; DATABASE ENTRY DATE: - - -
 ; US-09-756-526A-3

Qy 1615 TTGGTTTATTACAAAGTCAGGGGTTAGAGTAACTGTGAAACTCTTCA 1674
 ; Query Match Score 7.7%; Best Local Similarity 57.0%; Matches 385; Conservative 0; Mismatches 243; Indels 48; Gaps 3;

Db 1771 TTGGTTTATTACAAAGTCAGGGGTTAGAACTCTTCA 1830
 Qy 1675 CAATCTTACATTAGATTCCTGATACTGCTGAAATACTCTTCA 1734
 Db 1831 CAATCTTACATTAGATTCCTGATACTGCTGAAATACTCTTCA 1890
 Qy 1735 ATATCTCTTACAACTACCGAGGTTAGGAAATACCCCTAACAGACTTT 1794
 Db 1891 ATATCTCTTACAACTACCGAGGTTAGGAAATACCCCTAACAGACTTT 1950
 Qy 213 AGA--CAAACAGATGATGACAACTTATTAAATGGAGAAATTTTGTGATACACC 269
 Db 1353 AGATCCTAAACAAAAAAATTGGTCATATTATGAACACGGAAAGACCTTTAAATCAAAC 1412
 Qy 270 GTTAACAGAAAGCATAAACAGCTAAAGTACAAACTTGTAGAGTAACTATT 329
 Db 1413 AATTTCTACAGCTGTAAAGAAATGCATTAGCTCTAATGGTTAARGATGTATT 1472
 Qy 330 ACAAAAGCTATAATTACAGCATTAGTGTAGTGGAGAAATTAAAAGACTAACAGCTCTGG 389
 Db 1473 AACCTACTATGAAAGGATTAAATGATGGAAAGAAATCCAGTGCAATACTGCCAG 1532
 Qy 390 ATTACACCATTATGCGATTACACAACTGCTCTGACTCTTAAATAAGTGTGAGAA 449
 Db 1533 ATTGTGATCATAGA 1556
 Qy 450 TGTTGACAACTGATTGTTATTCGAGAATACTGGTTCCAACCTTAAAGCT 509
 Db 1557 CGCTTATTCGAATTGTGACANTATGCCAACACTCCACGATGACACATT 1616
 Qy 510 ATTACTACCTATTATGCSAAGCTGCTPAATTTCATTAAATTACACAGGTGC 569
 Db 1617 ATTATTAAGTGTGATACAGAAGTGCALATTACATTGAAATTGATTCAGGGT 1676
 Qy 570 TGAATGGCTGATGATGGAGATAACATCCTCACAAATTGACCTAATGCTGG 629
 Db 1677 ACBATTGCGGATCATGGATGCGATCACCAATTGCAATT 1727
 Qy 630 AACATCAGATGACTATTATAAACTTTAAAGAAATACTAAATATGAACTATTG 689
 Db 1728 GTCATGAGTACTTATGAGACCTATGGTATATAATGAAAGTATTAAATTG 1787
 Qy 690 TGCAATAACCTATAGAGAAAGCTAAATAACCTGAAACCTTAATGAGTGGAG 749
 Db 1788 CACCAAGCATACCTAAAGGATTGATCACCTPAGATGAGAAATTACATGGGA 1847
 Qy 750 TATATTTAATGATGATTCGAGAAGATAATGACTTACTGTTGATCTCAATT 809
 Db 1848 TGCTTAAACATCTGTCGAGAATGACCTTATTGTTGATCTTGCAACTT 1907
 Qy 810 TTCTTTATGATA 825
 Db 1908 TTCTTTATGATA 1923

RESULT 4
 US-09-756-526A-3
 Sequence 3, Application US/09756526A
 PARENT NO. US2003015005A1
 GENERAL INFORMATION:
 APPLICANT: Jana, Wojciechowska
 APPLICANT: Evgeny, Lewitin
 APPLICANT: Ludmila, Revina
 APPLICANT: Igor, Zalunin
 TITLE OF INVENTION: NOVEL DELTA-ENDOTOXINS AND NUCLEIC ACID SEQUENCES CODING THEREFOR
 FILE REFERENCE: S-30913A
 CURRENT APPLICATION NUMBER: US/09/756,526A
 CURRENT FILING DATE: 2001-01-08
 PRIOR APPLICATION NUMBER: US 60/175,158
 PRIOR FILING DATE: 2000-01-07
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 3
 LENGTH: 4896
 TYPE: DNA
 ORGANISM: *Bacillus thuringiensis*
 FEATURE: source
 NAME/KEY: source
 LOCATION: (1)..(496)
 OTHER INFORMATION: *Bacillus thuringiensis* supsp. *finitimus* strain VKPM B-1161 (taxon
 OTHER INFORMATION: :29337
 NAME/KEY: CDS
 LOCATION: (1129)..(4458)
 OTHER INFORMATION: product: Cry28Aa1 delta-endotoxin
 PUBLICATION INFORMATION:
 AUTHORS: Wojciechowska, et al.
 TITLE: Two novel delta-endotoxin gene families cry26 and cry28 from *Bacillus*
 TITLE: *thuringiensis* ssp. *finitimus*
 JOURNAL: FEBS Lett.
 VOLUME: 453
 ISSUE: 12
 PAGES: 46-48

RESULT 5
 US-10-345-020-3
 Sequence 3, Application US/10345020
 Publication No. US2003015018A1
 GENERAL INFORMATION:
 APPLICANT: Jana, Wojciechowska
 APPLICANT: Evgeny, Lewitin
 APPLICANT: Ludmila, Revina
 APPLICANT: Igor, Zalunin
 APPLICANT: Galina, Chestukhina
 TITLE OF INVENTION: NOVEL DELTA-ENDOTOXINS AND NUCLEIC ACID SEQUENCES CODING THEREFOR
 FILE REFERENCE: S-30913B
 CURRENT APPLICATION NUMBER: US/10/345,020
 CURRENT FILING DATE: 2003-01-15
 PRIOR APPLICATION NUMBER: US 60/175,158
 PRIOR FILING DATE: 2000-01-07

NUMBER OF SEQ ID NOS: 5
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 3 LENGTH: 4896
 TYPE: DNA
 ORGANISM: *Bacillus thuringiensis*
 FEATURE:
 NAME/KEY: source
 LOCATION: (1)..(4896)
 OTHER INFORMATION: *Bacillus thuringiensis* supsp. *finitimus* strain VKPM B-1161 (taxon
 OTHER INFORMATION: 29337
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1129)..(4458)
 OTHER INFORMATION: product: Cry28Aai delta-endotoxin
 PUBLICATION INFORMATION:
 AUTHORS: Wojciechowska, et al.
 TITLE: Two novel delta-endotoxin gene families cry26 and cry28 from *Bacillus*
 JOURNAL: FEBS Lett.
 VOLUME: 453
 ISSUE: 12
 PAGES: 46-48
 DATE: 1999-06-18
 US-10-345-020-3

Query Match 7.7%; Score 161.2; DB 6; Length 4896;
 Best Local Similarity 57.0%; Pred. No. 3..3e-19; Indels 48; Gaps 3;
 Matches 385; Conservative 0; Mismatches 243; Feature: DNA

Qy 153 AGGTGCTATAATATATCTTGTACCCATACTGTCTTGCGGCCGGAGAAC 212
 Db 1293 AGGTGTCGACTATATATTGGAAACCTGGCTCCGTTGGCTGATCAGAGGA 1352
 Qy 213 AGA--CAGTGGACACAATTATAAAATGGGAAATTTTTGTTGATACAC 269
 Db 1353 AGATCCAAAATTTGTCAAGATTAGAACACGGAGACCTTTAAATCAAC 1412
 Qy 270 GTAAACAGAAAGATAAACAGTAAGTACAAACTTAGAGGATTAGCATAATT 329
 Db 1413 AATTCTAACGTGTAAAGAAATAGCATATTAGCTCACTAAATGGTTAAAGATGTATT 1472
 Qy 330 ACAAAAGCTATAACAGCTTATAGCTGTTAGGAAATAAAAGACTAACAGCTCTGG 389
 Db 1473 AAGTACTATGAGAGGATTATGTTATGTTGGAGAGAATCTGCAG 1532
 Qy 390 ATTACACCATTACATCGGATTAAACAGCTGACTCTAAATAGATTGGAA 449
 Db 1533 ATGGTATACAGATAGA-----GATTTGAAAA 1556
 Qy 450 TGTTCACATGATTATTGAGAAATACCTGGCTTCCACTGAACTTAAAGCT 509
 Db 1557 CGCTCATTCATTGAAAGCAATATGCCAACCTCCAGTGCACAT 1616
 Qy 510 ATTTACTCCATTATGCGCAAGCTGTAAATTCTCAAAAGTGC 569
 Db 1617 ATTATTAGTGTGTATAGCAAGCTGCAATTGAACTTGTCAAGTGT 1676
 Qy 570 TGAATTGGCTGTGAAATGGAACTGAGATACTACATCCCTCACAAATGGACCTAATGCTGG 629
 Db 1677 ACATTCGGGATCAATGAAATCGAGCAACACATCACCAT-----GTGAA 1727
 Qy 610 AACATCAGATGAACTTAAAGAAATATACCTAAATATAGTAACTATTG 689
 Db 1728 GTCTACAGGTACTTATGACGAGCTATTGAAAGTATATTG 1787
 Qy 630 TGCRAAATACCTATAGAGGAGCTAAATAAATCTGAAAGCAGACCTAATAGATGG 749
 Db 1788 CACCAAGATACCTATAGGGATGAACTGAAATCTGAAATGCAATGGA 1847
 Qy 750 TATTTAAATGATTATGAGGATATGAACTTAACTGATGAACTATCGCTCAATT 809
 Db 1848 TGTTTATAACATACATCGGAAATGCTTAATGTTGATGCTGGCAACTT 1907

Qy 810 TTCTTTTATGATATA 825
 Db 1908 TCCTTTTATGATATA 1923

RESULT 6
 US-10-342-821-3
 Sequence 3, Application US/10342821
 Publication No. US20030154510A1
 GENERAL INFORMATION:
 APPLICANT: Jana, Wojciechowska
 APPLICANT: Evgeny, Lewitin
 APPLICANT: Ludmila, Revina
 APPLICANT: Igor, Zalunin
 APPLICANT: Galina, Chestuhthina
 TITLE OF INVENTION: NOVEL DELTA-ENDOTOXINS AND NUCLEAR ACID SEQUENCES CODING THEREFOR
 FILE REFERENCE: S-30913C
 CURRENT APPLICATION NUMBER: US/10/342,821
 CURRENT FILING DATE: 2003-01-15
 PRIOR APPLICATION NUMBER: US 60/175,158
 PRIOR FILING DATE: 2000-01-07
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 3 LENGTH: 4896
 TYPE: DNA
 ORGANISM: *Bacillus thuringiensis*
 FEATURE:
 NAME/KEY: source
 LOCATION: (1)..(4896)
 OTHER INFORMATION: *Bacillus thuringiensis* supp. *finitimus* strain VKPM B-1161 (taxon
 OTHER INFORMATION: 29337
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1129)..(4458)
 OTHER INFORMATION: product: Cry28Aai delta-endotoxin
 PUBLICATION INFORMATION:
 AUTHORS: Wojciechowska, et al.
 TITLE: Two novel delta-endotoxin gene families cry26 and cry28 from *Bacillus*
 JOURNAL: FEBS Lett.
 VOLUME: 453
 ISSUE: 12
 PAGES: 46-48
 DATE: 1999-06-18
 US-10-342-821-3

Query Match 7.7%; Score 161.2; DB 6; Length 4896;
 Best Local Similarity 57.0%; Pred. No. 3..3e-19; Mismatches 243; Indels 48; Gaps 3;
 Matches 385; Conservative 0; Mismatches 243; Feature: DNA

Qy 153 AGGTGCTATAATATCTTGTACCCATACTGTCTTGCGGCCGGAGAAC 212
 Db 1293 AGGTGTCGACTATATATTGGAAACCTGGCTCCGTTGGCTGATCAGAGGA 1352
 Qy 213 AGA--CAGTGGACACAATTATAAAATGGGAAATTTTTGTTGATACAC 269
 Db 1353 AGATCCAAAATTTGTCAAGATTAGAACACGGAGACCTTTAAATCAAC 1412
 Qy 270 GTAAACAGAAAGATAAACAGTAAGTACAACTTAGAGGATTAGCATAATT 329
 Db 1413 AATTCTAACGTGTAAAGAAATAGCATATTAGCTCACTAAATGGTTAAAGATGTATT 1472
 Qy 330 ACAAAAGCTATAACAGCTTATAGCTGTTAGGAAATAAAAGACTAACAGCTCTGG 389
 Db 1473 AAGTACTATGAGAGGATTATGTTATGTTGGAGAGAATCTGCAG 1532
 Qy 390 ATTACACCATTACATCGGATTAAACAGCTGACTCTAAATAGATTGGAA 449
 Db 1533 ATGGTATACAGATAGA-----GATTTGAAAA 1556
 Qy 450 TGTTCACATGATTATTGAGAAATACCTGGCTTCCACTGAACTTAAAGCT 509
 Db 1557 CGCTCATTCATTGAAAGCAATATGCCAACCTCCAGTGCACAT 1616
 Qy 510 ATTTACTCCATTATGCGCAAGCTGTAAATTCTCAAAAGTGC 569
 Db 1617 ATTATTAGTGTGTATAGCAAGCTGCAATTGAACTTGTCAAGTGT 1676
 Qy 570 TGAATTGGCTGTGAAATGGAACTGAGATACTACATCCCTCACAAATGGACCTAATGCTGG 629
 Db 1677 ACATTCGGGATCAATGAAATCGAGCAACACATCACCAT-----GTGAA 1727
 Qy 610 AACATCAGATGAACTTAAAGAAATATACCTAAATATAGTAACTATTG 689
 Db 1728 GTCTACAGGTACTTATGACGAGCTATTGAAAGTATATTG 1787
 Qy 630 TGCRAAATACCTATAGAGGAGCTAAATAAATCTGAAAGCAGACCTAATAGATGG 749
 Db 1788 CACCAAGATACCTATAGGGATGAACTGAAATCTGAAATGCAATGGA 1847
 Qy 750 TATTTAAATGATTATGAGGATATGAACTTAACTGATGAACTATCGCTCAATT 809
 Db 1848 TGTTTATAACATACATCGGAAATGCTTAATGTTGATGCTGGCAACTT 1907

Qy 810 TTCTTTTATGATATA 825
 Db 1908 TCCTTTTATGATATA 1923

1557	CGGTCAATTGTAAGCAATATGCCAACACTCCGAACGTTGGCACATT	1616	
510	ATTACTACTTATTGCCCCAAGCTGCTATTTCATTAACAAAGGTGC	569	
1617	ATTATTAGTTGCTATAAGGTGAATTATTACATTCAGGTGT	1676	
570	TGATTGCTGATGCAATGGAAATGCAATCCTTCACAAATTGAACTTA	629	
1677	ACATTGCGGATCAATGGAAATGCAACCATTCACATT	1727	
630	AACATCAGTAGACTATTAAAGAAAATACCTAAATAGTAACATTG	689	
1728	GTCATCAGGTACTTATTAGCAGGCTATGGTATATTGAAAGTATTAT	1787	
690	TGCAAATACCTATAGAGAACTTCAAACTTGAACTTAAATGAGATGG	749	
1788	CACCAAGACATACCAAAAGGTGAATCACCTAAAGATCAGAAAAA	1847	
750	TATATTATGATTATCGAGGATATGACTATTACTGTATAGTAACTAT	809	
1848	TGCTTAAACACATATCGTGAGAAATGACCTTAATTGTATGGCATCT	1907	
810	TTCCTTTATGATAAA 825		
1908	TCCCTTTATGATAAA 1923		
<hr/>			
RESULT 7			
JS-10-311-455-2128/C			
Sequence 2128, Application US/10311455			
Publication No. US20030143606A1			
GENERAL INFORMATION:			
APPLICANT: OLEK, Alexander			
APPLICANT: PIPENBROCK, Christian			
APPLICANT: BERLIN, Kurt			
TITLE OF INVENTION: Cytosine methylation			
FILE REFERENCE: 5013_1014			
CURRENT FILING DATE: 2002-12-16			
PRIOR APPLICATION NUMBER: PCT/EP01/07537			
PRIOR FILING DATE: 2001-07-02			
PRIOR APPLICATION NUMBER: DE 10032529.7			
PRIOR FILING DATE: 2000-06-30			
PRIOR APPLICATION NUMBER: DE 10043826.1			
PRIOR FILING DATE: 2000-09-01			
NUMBER OF SEQ ID NOS: 2424			
SEQ ID NO: 2128			
LENGTH: 15548			
TYPE: DNA			
ORGANISM: Artificial Sequence			
FEATURE: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)			
US-10-311-455-2128			
Query Match Score 5.6%; Length 15548;			
Best Local Similarity 43.6%; Fred. No. 6.2e-11;			
Matches 819; Conservative 0; Mismatches 1040; Indels 18; Gaps 6;			
SEQUENCE ALIGNMENT			
Qy	218 AACAGTATGGACACAAATTGTAAGTCAACTTGGAGAAATTGTTGATACACCGTAAACAG 277	Db	13398 ATAAATAACATATAGCTGCAATTAATAGCTAAATATATAAAATACAGTAAATACAGT 13339
Qy	278 AAAGCATAAACAGTAAAGTCAACTTGGAGAAATTGTTGATACACCGTAAACAG 337	Db	13338 CTAATAATATATATATAATTCAGCTATAAAATATCTAAATATATATATACAGT 13279
Qy	338 ATAATACAGCTTATGATGTTGGAGAAAATAAAGACTACAGTAAATACAGTAAATACAGT 397	Db	13278 AAAATAATACATATAATATATAATATATAATATATAATATATAATATATAATATA 13219
Qy	398 CATCATCGCAATTACACAAAGTGCCTTGAATCTTAAATGCAATATAGTGAATGTCACA 457	Db	1465 TATACAGGTGCAATTACACAAAGTGCCTTGAATCTTAAATGCAATATAGTGAATGTCACA 1524

Db	1874	CAAGACCTAATAATACCTACAGATTAAATAGAAGAGTTAGATAAAAGATC	1933	Qy	573	ATGGGTCATGATGGAGATGAGATATACATCCCTACAAATTGAACTTAAATGCTGGAAC	632
Qy	1839	-TTGCCAATTCCAAAGTAGAAGTACATTCCTTAATCGAACATGACATTATATA	1897	Db	1715126	TAAAATA	1715067
Db	1934	CTTTGTGATCAATTGTACCGATGGATTPATCTCTAACTGTATCATGCTTTC	1993	Qy	633	ATCAGGAGACTATTAACTTTAAAGAAATTACCTAAATAGTAACTATGTTGTC	692
Qy	1898	ATCGTGAGATG--ATCAAATTCATTAACTGTGATAAAATGGATTATACCA	1954	Db	1715066	TAATA	1715007
Db	1994	AACCTTAAACATGACTCTTAACTGTGATTTGATGTTACGATTCGAATTCCA	2053	Qy	693	AAATACTTATAGAAGAGGACTAAATAACTCGAAACCTAAATCGAGTGGAGAT	752
Qy	1955	TTACTTCCCTCTGTAGCCAAATTAGAGAAAACAAATTAGAAGACTTACACAAA	2014	Db	1715006	AAATA-TAT	1714948
Db	2054	TCACTCAATTGCTGATTAGTGAGAGAACCAAATTAGATCAGGAGAAGTTG	2113	Qy	753	ATTTATGATTATCGAGAAGTATATGACDPATTACTGTATTAGATGACTATCGCTCAATTTC	812
Qy	2015	TAATACATTTCATCAAAATCATACAAANAACTTAAATAGAACCCAAACTATG	2074	Db	1714947	ACAAATATATATACAAATAATATATATATATATATATATAATAATAATAATAATA	1714888
Db	2114	TGAATGCACTGTTPACAATGACCGAAAPATGCACTAACATTGGAAACGATATTG	2173	Qy	813	TTTTATGATATAAAGAGATACTACAAAGATTCATAGGAAAGATGGGCTTAAACTGA	872
Qy	2075	ATATTGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA	2085	Db	1714887	TAATA	1714828
Db	2174	ACATAGATCNA	2184	Qy	873	ACTTAACAGAAATTACAAACTGAAATAAATTGACCGTCTACTTACCTGAAAT	932
Qy	9	US-10-312-841-1/C		Qy	933	TCAACCCAATCTGCCTTAACTGTTAACTTAACTTAACTTAACTTAACTA	992
		Sequence 1, Application US/10312841		Db	1714767	TATCATATAAAATTATATATATATATATATATATATATATATATATA	1714708
		Publication No. US20030186277A1		Qy	993	ATTTATGAGAACTTATATTATACAAAAAATGAAAGTACGGAAATCGTTTAACTG	1052
		GENERAL INFORMATION:		Db	1714707	TAATA	1714649
		APPLICANT: Epicoromics AG		Qy	1053	TATTGGAAATCTGATAAGTCTACTATGCTTACCTATGCTTACCAAGAACTTATATGGAGA	1112
		FILE REFERENCE: E011208/WO		Db	1714648	TATATAATA	1714589
		CURRENT APPLICATION NUMBER: US/10/312,841		Qy	1113	ARGAACAGGTCCACCCACACAAAPAACTTTAACTACATTGAACTTATAAGTCTCAAT	1172
		CURRENT FILING DATE: 2002-12-30		Db	1714588	TAATA	1714529
		NUMBER OF SEQ ID NOS: 2		Qy	1173	---TGTAACTGTAGACAGTAACTCTACTTCCCCTTCCPAACTATACCTTACAT	1229
		SEQ ID NO: 1		Db	1714528	ATA	1714469
		LENGTH: 3673778		Qy	1230	TAATCGAAATTGAACTTTATTAATTAATTAATTAATTAATTAATTAATTAATTA	1289
		TYPE: DNA		Db	1714468	TATATAATA	1714409
		ORGANISM: Artificial Sequence		Qy	1350	TAACCCAAATTATTCACCAATTGTTACAGCTTACATGCTTATAGTCATATTTCAT	1409
		FEATURE: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)		Db	1714348	TA	1714290
		FEATURE:		Qy	1290	GGGGAAATTPTCTATGATAAAAAPAACTGATTTCATTCTGTAAAAAGAGACTG	1349
		NAME/KEY: unsure		Db	1714408	ATATAAAATATATATATATATATATATATATATATATATATATA	1714289
		LOCATION: (3294164)		Qy	1410	CCAGTTTCCTTATTAAATTCTCTTAAATTTGCTAAATATATATATATA	1469
us-10-312-841-1				Db	1714408	TATATATAATATATATATATATATATATATATATATATATATA	1714229
		Query Match Score: 99.2%; DB: 6; Length: 3673778;		Qy	1530	ATTACATGATCCAGCAATTGAGTAACTCTGTTACAGCTTGTAACTTAACT	1589
		Best Local Similarity: 43.7%; Pred. No. 9.6e-07; Mismatches: 811; Conservative: 0; Gaps: 8;		Db	1714169	AAAATA	1714110
		Matches: 811; Gaps: 8; Indels: 15; Mismatches: 1028;		Qy	1590	AGGACCTGGTCACTAGGAGCAACCTGGTTTATACAGCTAAGGGCTTAGAGAT	1649
				Db	1714109	TAAATA	1714050
				Qy	1650	TACATGTAGAACTCTCTACACAACTTACATGATCAGCTAAGCTGATCAGCTA	1706

RESULT 15
 US-10-825-751-7
 Sequence 7, Application US/10825751
 Publication No. US20040194165A1
 GENERAL INFORMATION:
 APPLICANT: Payne, Jewel
 APPLICANT: Sick, August J.
 TITLE OF INVENTION: Novel *Bacillus thuringiensis* Isolate Active Against Lepidopteran Pests, and Genes Encoding Novel Lepidopteran-Active Toxins
 FILE REFERENCE: MA-43CDP2D4
 CURRENT APPLICATION NUMBER: US/10/825, 751
 CURRENT FILING DATE: 2004-04-16
 PRIOR APPLICATION NUMBER: US 09/837, 961
 PRIOR FILING DATE: 2001-04-19
 PRIOR APPLICATION NUMBER: US 09/521, 344
 PRIOR FILING DATE: 2000-03-09
 PRIOR APPLICATION NUMBER: US 08/933, 891
 PRIOR FILING DATE: 1997-09-19
 PRIOR APPLICATION NUMBER: US 08/356, 034
 PRIOR FILING DATE: 1994-12-14
 PRIOR APPLICATION NUMBER: US 08/210, 110
 PRIOR FILING DATE: 1994-03-17
 PRIOR APPLICATION NUMBER: US 07/865, 168
 PRIOR FILING DATE: 1992-04-09
 PRIOR APPLICATION NUMBER: US 07/451, 261
 PRIOR FILING DATE: 1989-12-14
 PRIOR APPLICATION NUMBER: US 371, 955
 PRIOR FILING DATE: 1989-06-27
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: Patentin version 3.2
 SEQ ID NO 7
 LENGTH: 3522
 TYPE: DNA
 ORGANISM: *Bacillus thuringiensis*
 us-10-825-751-7

Query Match Score 3.8%; Score 79.6; DB 8; Length 3522;
 Best Local Similarity 53.3%; Pred. No. 0; 0.00024;
 Matches 212; Conservative 0; Mismatches 159; Indels 27; Gaps 1;

Qy	ATACGATTGAGAATGTTCAATGACTTATTCGAGAAATACCTGGTTCCAACCTGAA	495
Db	ATTCGATTGCTATACTAGACGCCGCTTAATAACGGATAAAATTATTCACCTTACA	447
Qy	ACTTATANACGTATTACTACCTATTA	555
Db	AGTTTGAAATCCTCTTATCGGTCTATGTCAGCGGCATAATTACATTATCACTA	507
Qy	TTCACACAGGTCTGAATGGCTGATGAAATCGAGATACTCCACAAAT	615
Db	TTAAGAGAGCTATCCTGGACACATACTACAGGTTAGGTCTATGTTAATAT	567
Qy	GAACCTAATGCTGAAACATCAGTCACTTATAAACCTTAAAGAAATAACCTAA	675
Db	C-----ATTATAATGAGATAATAATCTATTATCATAGA	600
Qy	TATAGTAATATGTCATAACCTATAGAGGACTAATAAACCTCGAACGACCT	735
Db	TATACGAAACATGTTGGACACATACTACAGGTTAGGTCTATGTTAATAT	660
Qy	AATATGAGATGGAGATATTAACTGAGAGATAATGACTTACCTGTTAATAT	795
Db	ACTGACAAATGGCAAGATCAATCAGTTAGGAGATTAACACTCTGTATZAGAT	720

Qy 796 ACTATCGCTCAATTTCCTTTATGATATAAGAGATA 833
 Db 721 ATCGTTCCTCTTTCGAACTACGATGTTGAGACATA 758

Search completed: February 15, 2006, 05:12:27
 Job time : 1555 secs

Result No.	Score	Query Match	Length	DB ID	Description	SUMMARIES	
1	75.6	3.6	1959	11	US-11-192-801-1 Sequence 1, Appli	Qy	Query Match 3.6%; Score 75.6; DB 11; Length 1959;
2	71.8	3.5	1959	11	US-11-192-801-3 Sequence 3, Appli	Qy	Qy 507 ACTTTTCAGGAAAGTCATTCTCAATCCATCGTATTGCAAC 566
3	71.4	3.4	171486	11	US-11-121-086-05 Sequence 105, Appli	Qy	Qy TTATAAACGCTATTACTACCTATTATGGCAAAGCTGTAATTCTTAATTT 557
4	71.4	3.4	173602	11	US-11-121-086-25 Sequence 25, Appli	Qy	Qy 567 ATTCCAGTGCTGTCTACCAACATATGCACAACTGCAAC 626
5	65.2	3.1	194553	11	US-11-098-086-03 Sequence 97, Appli	Db	Db 558 ACAAAAGGTCGCTGAATTGCTGATGAAATGCAATCCTTCACAAATTGA 617
6	65	3.1	130504	11	US-11-121-086-96 Sequence 96, Appli	Db	Db 627 AAAAGATGCTCAAGTTTTGAGAAGATGG-----GG 659
7	63.8	3.1	171486	11	US-11-121-086-105 Sequence 105, Appli	Qy	Qy 559 ACAAAAGGTCGCTGAATTGCTGATGAAATGCAATCCTTCACAAATTGA 617
8	61.8	3.0	173602	11	US-11-121-086-25 Sequence 25, Appli	Qy	Qy 567 ATTCCAGTGCTGTCTACCAACATATGCACAACTGCAAC 626
9	60.8	2.9	130504	11	US-11-121-086-96 Sequence 96, Appli	Db	Db 558 ACAAAAGGTCGCTGAATTGCTGATGAAATGCAATCCTTCACAAATTGA 617
10	59.4	2.8	158692	11	US-11-121-086-30 Sequence 30, Appli	Qy	Qy 559 ACAAAAGGTCGCTGAATTGCTGATGAAATGCAATCCTTCACAAATTGA 617
11	58.6	2.8	2031	11	US-11-098-086-03 Sequence 51, Appli	Db	Db 558 ACAAAAGGTCGCTGAATTGCTGATGAAATGCAATCCTTCACAAATTGA 617
12	58.6	2.8	2031	11	US-11-058-086-96 Sequence 83, Appli	Qy	Qy 559 ACAAAAGGTCGCTGAATTGCTGATGAAATGCAATCCTTCACAAATTGA 617
13	58.6	2.8	2031	11	US-11-108-089-51 Sequence 51, Appli	Db	Db 558 ACAAAAGGTCGCTGAATTGCTGATGAAATGCAATCCTTCACAAATTGA 617
14	58.6	2.8	2031	11	US-11-108-089-83 Sequence 83, Appli	Qy	Qy 559 ACAAAAGGTCGCTGAATTGCTGATGAAATGCAATCCTTCACAAATTGA 617
15	58.6	2.8	2031	11	US-11-224-024-51 Sequence 51, Appli	Db	Db 558 ACAAAAGGTCGCTGAATTGCTGATGAAATGCAATCCTTCACAAATTGA 617
16	58.6	2.8	2031	11	US-11-224-024-83 Sequence 83, Appli	Qy	Qy 559 ACAAAAGGTCGCTGAATTGCTGATGAAATGCAATCCTTCACAAATTGA 617
17	57.4	2.8	2028	11	US-11-058-072-39 Sequence 71, Appli	Db	Db 558 ACAAAAGGTCGCTGAATTGCTGATGAAATGCAATCCTTCACAAATTGA 617
18	57.4	2.8	2028	11	US-11-058-072-71 Sequence 39, Appli	Qy	Qy 559 ACAAAAGGTCGCTGAATTGCTGATGAAATGCAATCCTTCACAAATTGA 617
19	57.4	2.8	2028	11	US-11-108-089-39 Sequence 71, Appli	Db	Db 558 ACAAAAGGTCGCTGAATTGCTGATGAAATGCAATCCTTCACAAATTGA 617
20	57.4	2.8	2028	11	US-11-108-089-71 Sequence 39, Appli	Qy	Qy 559 ACAAAAGGTCGCTGAATTGCTGATGAAATGCAATCCTTCACAAATTGA 617
21	57.4	2.8	2028	11	US-11-224-024-39 Sequence 39, Appli	Db	Db 558 ACAAAAGGTCGCTGAATTGCTGATGAAATGCAATCCTTCACAAATTGA 617

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
OM nucleic - nucleic search, using bw model
Run on: February 15, 2006, 00:38:27 ; Search time 427 Seconds
(without alignments)
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Perfect score: 2085
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Searched: 6240305 seqs, 449581930 residues
Total number of hits satisfying chosen parameters: 12480610
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Published Applications NA_New:
 1: /cgn2_6/ptodata/1/pubbra/US08_NEW PUB.seq:
 2: /cgn2_6/ptodata/1/pubbra/US06_NEW PUB.seq:
 3: /cgn2_6/ptodata/1/pubbra/PCT_NEW PUB.seq:
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 7: /cgn2_6/ptodata/1/pubbra/US10_NEW PUB.seq:
 8: /cgn2_6/ptodata/1/pubbra/US11_NEW PUB.seq:
 9: /cgn2_6/ptodata/1/pubbra/US11_NEW PUB.seq:
 10: /cgn2_6/ptodata/1/pubbra/US11_NEW PUB.seq:
 11: /cgn2_6/ptodata/1/pubbra/US11_NEW PUB.seq:
 12: /cgn2_6/ptodata/1/pubbra/US60_NEW PUB.seq:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
US-11-192-801-1
; Sequence 1, Application US-11-192-801-1
; Publication No. US20050273882A1
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/11/192,801
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: US/10/232,665
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US/09/377,466
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1959
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: (1..(1956)
; OTHER INFORMATION: Describing nucleotide sequence encoding a Cry3Bb1
; OTHER INFORMATION: Occurring nucleotide sequence naturally occurring amino acid sequence
US-11-192-801-1

Query Match 3.6%; Score 75.6; DB 11; Length 1959;
Best Local Similarity 52.5%; Pred. No. 9.2e-06;
Matches 21.; Conservative 0.; Mismatches 164.; Indels 27.; Gaps 1.; Other information: amino acid sequence

Qy 438 ACGATTGAGAATGTCACATGATTTATTGAGAAATAACCTGGTTCCAACTGAAAC 497
Db 507 ACTTTTCAGGAAAGTCATTCTCAATTCATCGTATTGCAAC 566

Qy 498 TTATAAACGCTATTACTACCTATTATGGCAAAGCTGTAATTCTTAATTTATT 557
Db 567 ATTCCAGTGCTGTCTACCAACATATGCACAACTGCAAC 626

Qy 61.8 ACCTAATGTCGGAACATCGATGACTTAACTTTAACAGAAAATAACCTAAATA 677
 Db 66.0 ATATTCCTCAAGATGTGTGTTACAGACATAACACACATA 719

Qy 67.8 TAGTAACATTGTGCAAATAACCTPATAGAAGGACTTAATAACCTCGAAACGAACTAA 737
 Db 72.0 CACTGACCATTGTGTTAAATGGTAAATCTGGATTAATGGTTAACGGTTCACATTA 779

Qy 73.8 TATGAGATGGAGTATTTATGATTATGAAAGATATGACTTAACTGTGTTAGATAC 797
 Db 78.0 TGATGCATGGTCGAATTAAACCGTTTCGCAAGAATGACTTAACTGTGTTAGATC 839

Qy 79.8 TATCGCTCAATTCTTCTTATGATATAAGAGATAACAGA 839
 Qy 84.0 AATGTACTTCCATTITATGATTGGTTATACCTCAA 881

Db 84.0 AATTGTACTTCCATTITATGATTGGTTATACCTCAA 881

RESULT 3
 US-11-121-086-105/C ; Sequence 105, Application US/11-121-086
 ; Publication No. US20050266459A1 ; GENERAL INFORMATION:
 ; APPLICANT: POULSEN, TIM S. ; APPLICANT: NIELSEN, KIRSTEN V.
 ; TITLE OF INVENTION: NUCLEARIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
 ; FILE REFERENCE: 09138-6000-00000 ; CURRENT APPLICATION NUMBER: US/11-121-086
 ; CURRENT FILING DATE: 2005-05-04 ; PRIOR APPLICATION NUMBER: 60/567,570
 ; PRIOR FILING DATE: 2004-05-04 ; NUMBER OF SEQ ID NOS: 107
 ; SOFTWARE: Patentin version 3.3
 SEQ ID NO 105 ; LENGTH: 171486 ; TYPE: DNA ; ORGANISM: Homo sapiens

US-11-121-086-105
 Query Match 3.4%; Score 71.8; DB 11; Length 171486;
 Best Local Similarity 44.1%; Pred. No. 9.1e-05;
 Matches 580; Conservative 0; Mismatches 717; Indels 18; Gaps 6;

Qy 775 ATGAGCTATCTGTGATAGATCTTGCGCTATTTCTTGATATAGAGATAC 834
 Db 17682 ATCTPATATAATATAATATAATATAATATAATCTCPATAATATAATATAA 1762
 Qy 835 AAAGATTCATAGGAAATAAGTGGCATTA-AAGTGAACCTACAGAGAAATTATAC 893
 Db 17622 ATATATTTATATATCTCTATATATATATATATATATATATATATATATAT 1756

Qy 894 AACTGAATAAATTGACCGCTCTACCTTACCTTGAAATTGACCCATTCTCGCTTATAT 953
 Db 17562 ATCTPATATAATATAATATCTATAATATAATCTATAATATAATATAATATA 1750

Qy 954 GGAAATTAATTTAACCGTCTAGGGTTGATTATTCATTTTACGTGACTTATT 1013
 Db 17502 TCTATAATATAA-----ATCTPATATAATATAATCTATAATATAATATA 1745

Qy 1014 TTATACAAAATGAAAGTACGGGATCGTTAGTGGTATTGGAAATCGTAATAGATC 1073
 Db 17449 CTATATATATTTTATATATATATATATATATATATATATATATATATATAT 1739

Qy 1074 TACITATGCTACGACAGGAACCTGAAATTATATGGAGAAAGAACGGTCCACAC 1133
 Db 17389 TATATATATAATCTATAATATATATATATATATATATATATATATAATA 1733

Qy 1134 AAAACCTTATACCTTCAACTTCAACTTCAACTTCAACTTCAACTTCAACTTCA 1193
 Db 17329 TATTTATATATCTACAATAATATAATATAATATAATATATCTATAATATA 1727

Qy 1194 TCCPACTTCCCTTCCPACATACATCTTACAATTAATCAATTAATCAATTAAT 1253
 Db 17269 AAATATATAATATATTTATATCTATACTTATAATATATATATATATATATA 1721

Qy 1254 TAATTCACCTGTTACATTGTTACATTGTTACATTGTTACATTGTTACATTGTT 1313
 Db 17209 TCTATAATATAATATAATATATATATATATATATATATATATATATAATA 1715

Qy 1314 AACATGTTTCAATTCTGTTAACCTTCAACCTTCAACCTTCAACCTTCAACCTT 1373
 Db 17149 TATTTATATATCTATAATATAATATAATATAATATAATATAATATAATA 1709

Qy 1374 TTACCAAGCTATAATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1433
 Db 17093 TATTTATATAATATAATATAATATAATATAATATAATATAATATAATATA 1703

Qy 720 CACTGACCATTGTGCAATTGGTAAATGGTTAACGGTTCACACTTA 779
 Qy 73.8 TATGAGATGGAGTATTTATGATTATGAAAGATATGACTTAACTGTGTTAGATAC 797
 Qy 78.0 TGATGCATGGTCGAATTAAACCGTTTCGCAAGAATGACTTAACTGTGTTAGATC 839

Qy 79.8 TATCGCTCAATTCTTCTTATGATATAAGAGATAACAGA 839

Best Local Similarity 44.9%; Pred. No. 0.021; Indels 12; Gaps 4; Matches 394; Conservative 0; Mismatches 471;

Db	43426	ATTTAAATATAAATATAATTAACTTACATACATCATACTTATAAT--TT	43483
Qy	764	ATCGAGATATAAGACTTACTGTTAGATGACTATGCTTAATTCTTTTATGATA	823
Db	43484	AATCAACTATATAATTATATTATATTATATTATATTATATAAATGGAG	43543
Qy	824	TAAGAGATACAAGAGTCAATTAGGAAGATACTGGCATTAACACTAACAGAG	883
Db	43544	AATATAGTTATAATTAAATATAATTAAATATAATTAAATATAATTATAA	43603
Qy	884	AATTATTAACACTGAAATAATTGACGCTTACTACCTGTAATTCAACCCATC	943
Db	43604	TAAATATAATTATATTATAATTATAATTATAATTAGAAATACATATAATTATA	43663
Qy	944	TGCTATATTGGATTATTTACAGTTCAGGGCTTACGGCTTACGGCTTACGGT	1003
Db	43664	T-AATATTTATATTATATTATATTATATTATATTATGTATGATAATAATA	43722
Qy	1004	AACTTATTTTATCACAAAATGAAACCTACCGGAATGCTTAGTTGCTTATGGCAT	1063
Db	43723	TAATTAGTAATAATTATAATTATAATTATAATTATAATTATAATTATAAT	43782
Qy	1064	GTAATAGATCTACTATGTTACAGCAGGAACTGAAATTATGGAGAAGAACGGTC	1123
Db	43783	ATATAATTATAACATATGTTAAATACAAATATGTCATATTATGTTAAATATA	43842
Qy	1124	CACCCACACAAAAAC-----TTAAATACATTGAACTTAAAGFTCAATTGTAAC	1178
Db	43843	TTTACATATTATATGCAATTATTAACATATTAAATATTATPATPATAT	43902
Qy	1179	TGATAGACAGGAACTCTTACCTTACATTTACATTAAATCAAAAT	1238
Db	43903	TTATATTATATTAACTTACATTAAATTTTAAATTTATCAGTT	43962
Qy	1239	TGCACTTTTAAATTAATTTACCTAGTAAATTAACATATCAGCTGGGGAAATT	1298
Db	43963	TAA---TTATATTATTTATTATTTAAATTTAAATAGCATTAATTATPATTTAA	44019
Qy	1299	ATCPAATGATAAAAACACTGATTGTTACCTGAAAGCTGAAACCAT	1358
Db	44020	ATTAATATTAAACATTATTATAATGTTATTATATTATPATPATACAT	44079
Qy	1359	TATTAATCCAATGTTACCAAGCTATAATGTTACATTTCGCCAG----T	1414
Db	44080	TTTAAATACATTAAATTTACCTTAAATTTAAATATAATTATAGATAT	44139
Qy	1415	TTCTTTATTAAATTTACCTTAAATTTGCTTAAATTTACATAGTAT	1462
Db	44140	TTTTAAATATAAAATTATTTAAATATAATTATTTAAATTTATTTAT	44187

RESULT 10

US-11-121-086-30
Sequence 30, Application US/11121086
Publication No. US20050266459A1

GENERAL INFORMATION:

APPLICANT: POULSEN, TIM S.

APPLICANT: NIELSEN, KIRSTEN V.

TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

FILE REFERENCE: 09138_6000_00000

CURRENT APPLICATION NUMBER: US/11/121,086

CURRENT FILING DATE: 2005-05-04

PRIOR APPLICATION NUMBER: 60/567,570

PRIOR FILING DATE: 2004-05-04

NUMBER OF SEQ ID NOS: 107

LENGTH: 156692

TYPE: DNA

ORGANISM: Homo sapiens

Query Match 2.8%; Score 59.4; DB 11; Length 158692;

Qy	646	TATAACTTTAAAGAAATACTTAATAGTAACATATGCGAAATACCT-ATAG	704
Db	44054	TATTAACATATAAACTGTTATAATGTTATAAAATATAAACTGTGATAT	44113
Qy	705	AGAAGGACTRAATAACCTGAAACGACCTTATAGATGAGATAATTATGATA	764
Db	44114	ATGCAATTATATAATTATAACATGTGATAATGCAATTATAATGAA	44173
Qy	765	TGAAAGATATGACTTACTGTTAGATGACTATCGCTCAATTCTTATGATAT	824
Db	44174	TATGTTGATATGTCATATA-TATAAAATATGATAATGTTATTATA	44232
Qy	825	AAAGAGATAACAGATTAATAGGAGATACTGGCATTAAACTGACTTACAGAGA	884
Db	44233	AAATATGAAATATGTGATATGTGATAATTATAAAATATGAAATATGTGT	44292
Qy	885	AATTATACAACTGAAATAATTGACCGCTTACCTGAAATTCAACCAACT	944
Db	44293	ATATTATATATAATTATGAAATATGCTATGTTATTATAATGATAATG	44352
Qy	945	CGCTAT-----ATGGAAATATAATTAAACCGTTAGGCTTAACTTTTAA	999
Db	44353	TGCTATGTCTATATTATAAAATGAAATATGTGTATGTTAAATAATAAATA	44412
Qy	1000	GATGAACCTATTATAACAAATAAAATGAAACCTACGGGAATCTGTTAGCTGG	1059
Db	44413	TATGAAATATGTGATGTTGTTATGAAATATAAAATATGAAATATGTGT	44472
Qy	1060	AATGCTTAATGATCTACTTGTCTACGAGAACTGAAATTATGAGAAAGAAC	1119
Db	44473	ATATAAAATATGAAATATGTTGTTATTTATAAAATATGAAATATGTTGATA	44532
Qy	1120	GGTCACCCCCACACACAAACACTTTAAACATTGCTTACCTTAAAGTTGAACT	1179
Db	44533	TGCTATATTATAAAATATAAAATATGTTATTATAAAATATAAAATATAAAAT	44592
Qy	1180	GATGACAGAAGTAACCTCTACTCCCTTCTAACATACTTACATTAACTAAATT	1239
Db	44593	ATATAAAATTATTAATATTATGAAATATAAAATATAAAATTATGTTATATA	44652
Qy	1240	GAACTTTATTAATAATTACCTTACATTAACTTACATTAACTTACATTAACT	1299
Db	44653	ATATAAAATTATGAAATATGTTATTATAAAATATAAAATATAAAATATAAA	44712
Qy	1300	TCTTAATGTTAAATTTACACTGTTCTTAAATGCTTAAATGCTAACT	1359
Db	44713	TAATAATATAAAATATAAAATATAAAATATAAAATATAAAATATAAAAT	44772
Qy	1360	AT-----TATCCTAAATTGTTACCAAGCTATAATGTTATGCTTAACTCCAGT	1414
Db	44773	ATATGTTATTTATATAAAATATAAAATATAAAATATAAAATATAAAATATA	44832
Qy	1415	TTTCCTTTATTAATTATGTTCTTAAATGCTTAAATGCTTAAATGCTTAA	1474
Db	44833	TATACTATATAATGTTATATAAAATGCTTAAATGCTTAAATGCTTAA	44832
Qy	1475	CATTGGATGACACAGACTGTTCTTAAATGCTTAAATGCTTAAATGCTTAA	1511
Db	44893	GAAATATATGTTGAAATACCTTTCCTCTTAAATGCTTAAATGCTTAA	44929

RESULT 11

US-11-058-727-51
Sequence 51, Application US/11058727
Publication No. US20050261483A1

GENERAL INFORMATION:

APPLICANT: Andre R. Abad

APPLICANT: Ronald D. Flannagan

APPLICANT: Rafael Herrmann

APPLICANT: Theodore W. Kahn

Db	886	AATTATGACACGGCACGTAC	906
	RESULT 12		
	US-11-058-727-83		
	Sequence 83 , Application US/11058727		
	Publication NO. US20050261483A1		
	GENERAL INFORMATION:		
	APPLICANT: Andre R. Abad		
	APPLICANT: Rafael Herrmann		
	APPLICANT: Theodore W. Kahn		
	APPLICANT: Albert L. Lu		
	APPLICANT: Billy Fred McCutchen		
	APPLICANT: James K. Presnail		
	APPLICANT: James P.H. Wong		
	APPLICANT: Cao-Guo Yu		
	TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal Activity		
	FILE REFERENCE: 35718/287809		
	CURRENT APPLICATION NUMBER: US/11/058,727		
	CURRENT FILING DATE: 2005-02-15		
	PRIOR APPLICATION NUMBER: 60/391,786		
	PRIOR FILING DATE: 2002-06-26		
	PRIOR APPLICATION NUMBER: 60/460,787		
	PRIOR FILING DATE: 2003-04-04		
	PRIOR APPLICATION NUMBER: 10/606,320		
	PRIOR FILING DATE: 2003-06-25		
	NUMBER OF SEQ ID NOS: 134		
	SOFTWARE: FastSEQ for Windows Version 4.0		
	SEQ ID NO 51		
	LENGTH: 2031		
	TYPE: DNA		
	ORGANISM: Bacillus thuringiensis (mutated)		
	FEATURE:		
	NAME/KEY: CDS		
	LOCATION: (1) ... (2031)		
	US-11-058-727-51		
	Query Match Score 58.6; DB 11; Length 2031;		
	Best Local Similarity 46.9%; Pred. No. 0.017; Mismatches 294; Indels 36; Gaps 2;		
Qy	214 GCAAAACAGTATGGACAATTATAAAATGGGAAATTTTGGTGTATACACCGTTA 273		
Db	322 GAAAGACTCAATGGGAAATTATGGAAACAGTAGAGAAACTCATTAAATAAAATA 381		
Qy	274 AGAGAANGCATAAAACAGCTAANGGTTAACCTTAAGGTTAGACAAATTTACAA 333		
Db	382 GCAGAATATGCGAAGGAAATAAGGCCTTCGGAAATTAGAGGTTAGGTAA 441		
Qy	334 AGCTTATAACACCATAGATGATGGAAATTAAAAGGCTACAGCTCCGGATAA 393		
Db	442 TTATATTAACCTTAAGGTTAGGAAATTAGGTTAAATTACCAA 501		
Qy	394 CCACCATCATACGATTACAACAGCTGCGCTTGACTCTTAAATACGTTGGAATGTT 453		
Db	502 AATGGTTCCGGCAGCCCTAACAGATG-----TGCGAAATCGATTGAATCCTG 552		
Qy	454 CACAAATGTTTATTCGAAATAACCTGGTTCAACTGGAACCTTATAAAGCTTAA 513		
Db	553 GATAGTTTATTCGCAATATATGCCATCTCTTGTAGTGACAAATTGGAAGTACCATTC 612		
Qy	514 CTACCTATTATTCGCAAGCTGCTTAATTTCATTAAATTACACAAGTGTGAA 573		
Db	613 CTTACTGTTATCAATGCAATGCACTGGGATGGTCAACACT-----ACT 705		
Qy	574 TTGGCTGATGATGAACTTAAACTTCGAGATAATCATCCTTCACAAATGAAACCTAATGTGGTCAATT 672		
Db	706 ATTAAATACTATATGATCGTGTCAAATGAAACTTACTGCAAGATAATTCTGATCCTGTTA 765		
Qy	694 AATACCTATTAGAGAAGGCTAAATAAAACTTCGAAACGACCTTAATGAGTGGAGTATA 753		
Db	766 ACTGGTATGAACTGGTTAGAAAATTAAGGAGGCAAGGCTTAAACAATGGTGAC 825		
Qy	754 TTTAATGATTATGCAAGATAATGACTATTACTGTTAATGATACTACGCTGCTTAATTCTCT 813		
Db	826 TATAACCATTCTCGTAGAAATGACACTGGGTTTTAGATTTGTGCAATTCTCCA 885		
Qy	814 TTGATGACTTATAACCTTAAAGAAAATATACCTAAATACTTAAAGAAAAT 834		

Db 706 ATTAATAACTTATTGATCGTCAAATGAAACTACTGGAGAATATTCGTGATCACTGTGA 765
 Qy 654 AATACCTATAGAGGGCTTAATTAACCTCGAACGCCATTATCAGATCGAGATA 753
 Db 766 AATGGPATGAAACTGGTTAGCRAAAATTAAAGGCACGAGCCCTAAACAATGGGTGAC 825
 Qy 754 TTATGATGATTCGAGATATGACTATACGTATAAGTAACTGCTCAATTTCT 813
 Db 826 TATRACCATTCCCTGAGAACTGACAACTGGGTTTAGATGTTGTCATATTCCA 885
 Qy 814 TTTATGATATAAGAGATAC 834
 Db 886 AATTAGACACACGGCACGTAC 906

RESULT 13
 US-11-108-389-51
 Sequence 51, Application US/11108389
 Publication No. US2005026118BA1
 GENERAL INFORMATION:
 APPLICANT: Andre R. Abad
 APPLICANT: Ronald D. Flannagan
 APPLICANT: Rafael Herrmann
 APPLICANT: Theodore W. Kahn
 APPLICANT: Albert L. Lu
 APPLICANT: Billy Fred McCutchen
 APPLICANT: James K. Presnail
 APPLICANT: James F. H. Wong
 APPLICANT: Cao-Guo Yu
 TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal Activity

CURRENT APPLICATION NUMBER: US/11108,389
 CURRENT FILING DATE: 2005-04-18
 PRIOR APPLICATION NUMBER: 60/1391,786
 PRIOR FILING DATE: 2002-06-26
 PRIOR APPLICATION NUMBER: 60/460,787
 PRIOR FILING DATE: 2003-04-04
 PRIOR APPLICATION NUMBER: 10/506,320
 PRIOR FILING DATE: 2003-06-25
 NUMBER OF SEQ ID NOS: 134
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 51
 LENGTH: 2031
 TYPE: DNA
 ORGANISM: *Bacillus thuringiensis* (mutated)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1) . . . (2031)
 US-11-108-389-51

Query Match Score 58.6; DB 11; Length 2031;
 Best Local Similarity 46.9%; Pred. No. 0.017;
 Matches 291; Conservative 0; Mismatches 294; Indels 36; Gaps 2;

Qy 214 GACAAAACAGTATGGACAAATTATAATGGAGAAATTATGGACAAACTTACACGTTA 273
 Db 322 GAAAAGAGTCAATGGAAATTATGGCAAGTAGACAAACTTACACGTTA 381
 Qy 274 ACAGAAAGCATAAAACAGCTTAAAGTACACCTTAAAGGATTAGACAAATATTACAA 333
 Db 382 GCAGATATGGAGGATAAAAGCCTTGGAAATTAGACGTTAAATTACCAA 441
 Qy 334 AGCTATAATACGATTAGTATGGAGAAATTAAAGACTACAGTCCTGGGATA 393
 Db 442 TTATATCTAACTGGCTTGGAAATTCCATTGGAGTCAGGTGTTA 501
 Qy 394 CCACCATCATGAGATTACAAACAGCTGGCTTGACTTAAATAGATTGAGATGT 453
 Db 502 AATGGPTCCGGCAAGCCTTACGAGATG-----TGGAAATCGATTGAAATCTG 552
 Qy 454 CACAATGATTTATTCGAGAAATACTGGTTCCAACTTGAACCTTAAACGCTTATA 513

Db 553 GATAGTTTATTAGCGAAATATGCCCATTCTTAGGTGACAATTGAAATTGACCATTC 612
 Qy 514 CTACCTATTATGCGCAAGCPTGCTAAATTTCATTAAATTGAACTTAAACAAAGGTGGTGA 573
 Db 613 CTACTGATATGCAATTGCAACCTTCAATTGAGCCTGCAATT 672
 Qy 574 TTGGCTGATGAACTGGATGCGAGATAATCATCCTTCACAATTGAACTTAATGTTGAA 633
 Db 673 TTGGAGAGATGGATGGTCAACACT-----ACT 705
 Qy 634 TCAGATGACTTATTAACCTTAAAGAAATTATACCTAAATATGAACTATTGTCGA 693
 Db 706 ATTAAACTATGATCGTCAATTACTGAGAAATTCTGTGATCACTGTGCTA 765
 Qy 694 AATACCTATAGAGAAGGACTAATAAACTTCGAAACCTTAAATGAGTGGATA 753
 Qy 766 AATGGATGAAACTGGTTAGCAATTGGCTAAACATGGTTGAC 825
 Db 754 TTGATGATTATGGAGATATGACTTACTGTTAGATGACTATCGCTCAATTCTCT 813
 Db 826 TATPACCAATTCTGGAGAAATTGCAACTGGCTTATGAGTTGCTAATTCCCA 885
 Qy 814 TTTATGATATAAGAGATAC 834
 Db 886 AATATGACACACGGCACGTAC 906

RESULT 14
 US-11-108-389-83
 Sequence 83, Application US/11108389
 Publication No. US2005026118BA1
 GENERAL INFORMATION:
 APPLICANT: Andre R. Abad
 APPLICANT: Ronald D. Flannagan
 APPLICANT: Rafael Herrmann
 APPLICANT: Theodore W. Kahn
 APPLICANT: Albert L. Lu
 APPLICANT: Billy Fred McCutchen
 APPLICANT: James K. Presnail
 APPLICANT: James F. H. Wong
 APPLICANT: Cao-Guo Yu
 TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal Activity

CURRENT APPLICATION NUMBER: US/11108,389
 CURRENT FILING DATE: 2005-04-18
 PRIOR APPLICATION NUMBER: 60/1391,786
 PRIOR FILING DATE: 2002-06-26
 PRIOR APPLICATION NUMBER: 60/460,787
 PRIOR FILING DATE: 2003-04-04
 PRIOR APPLICATION NUMBER: 10/506,320
 PRIOR FILING DATE: 2003-06-25
 NUMBER OF SEQ ID NOS: 134
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 83
 LENGTH: 2031
 TYPE: DNA
 ORGANISM: *Bacillus thuringiensis*
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1) . . . (2031)
 US-11-108-389-83

Query Match Score 58.6; DB 11; Length 2031;
 Best Local Similarity 46.9%; Pred. No. 0.017;
 Matches 291; Conservative 0; Mismatches 294; Indels 36; Gaps 2;

Qy 214 GACAAAACAGTATGGACAAATTATAATGGAGAAATTATGGACAAACTTACACGTTA 273
 Db 322 GAAAAGAGTCAATGGAAATTATGGCAAGTAGACAAACTTACACGTTA 381
 Qy 274 ACAGAAAGCATAAAACAGCTTAAAGTACACCTTAAAGGATTAGACAAATATTACAA 333
 Db 382 GCAGATATGGAGGATAAAAGCCTTGGAAATTAGACGTTAAATTACCAA 441
 Qy 334 AGCTATAATACGATTAGTATGGAGAAATTAAAGACTACAGTCCTGGGATA 393
 Db 442 TTATATCTAACTGGCTTGGAAATTCCATTGGAGTCAGGTGTTA 501
 Qy 394 CCACCATCATGAGATTACAAACAGCTGGCTTGACTTAAATAGATTGAGATGT 453
 Db 502 AATGGPTCCGGCAAGCCTTACGAGATG-----TGGAAATCGATTGAAATCTG 552
 Qy 454 CACAATGATTTATTCGAGAAATACTGGTTCCAACTTGAACCTTAAACGCTTATA 513

Query Match Score 58.6; DB 11; Length 2031;
 Best Local Similarity 46.9%; Pred. No. 0.017;
 Matches 291; Conservative 0; Mismatches 294; Indels 36; Gaps 2;

Qy 214 GACAAAACAGTATGGACAAATTATAATGGAGAAATTATGGACAAACTTACACGTTA 273
 Db 322 GAAAAGAGTCAATGGAAATTATGGCAAGTAGACAAACTTACACGTTA 381
 Qy 274 ACAGAAAGCATAAAACAGCTTAAAGTACACCTTAAAGGATTAGACAAATATTACAA 333

Search completed: February 15, 2006, 03:05:11
Job time : 434 secs

RESULT 15
US-11-224-624-51
; Sequence 51, Application US/11/224624
; Publication No. US2006021096A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Andre
; APPLICANT: Dong, Hua
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert
; APPLICANT: McCutchen, Billy F.
; APPLICANT: Rice, Janet
; APPLICANT: Schepers, Eric
; APPLICANT: Wong, James
TITLE OF INVENTION: Genes Encoding Protein
TITLE OF INVENTION: Activity
FILE REFERENCE: 35718/297402
CURRENT APPLICATION NUMBER: US/11/224,624
CURRENT FILING DATE: 2005-09-12
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-05-25
PRIOR APPLICATION NUMBER: 10/746,914
PRIOR FILING DATE: 2003-12-24
NUMBER OF SEQ ID NOS: 143
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 51
LENGTH: 2011
TYPE: DNA
ORGANISM: *Bacillus thuringiensis* (mutated
FEATURE:
NAME/KEY: CDS